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US-09-009-913-1/c
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                                                                                                                                                                                                                                               Sequence 1, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AXYS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
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APPLICANT: WEBSTER,
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Patent No. 6365391
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Best Local Similarity
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TITLE OF INVENTION: USES
FILE REFERENCE: CL000862
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SOFTWARE: FastSEQ
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CURRENT FILING DATE: 3000-12-13
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                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
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APPLICATION NUMBER: US/09/009,913 FILING DATE: 21-JAN-1998
                                                                                                                                       COUNTRY:
                                                                                                                                                          STATE:
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285 Hamilton Ave, Suite 200
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100.0%; Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,232
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                            FILING DATE: 20-MAR-1991 PRIOR APPLICATION DATA:
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TELEFAX: 650-327-3231
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                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
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MANDEL, Jean-Louis
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09-SEP-1993
JMBER: US 07/638,518
04-JAN-1991
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US-08-650-598-1
US-08-99-252-108
PCT-US96-06352-108
PCT-US96-06352-102
PCT-US96-06352-102
PCT-US96-06352-95
US-08-833-95-95
US-08-833-95-95
US-08-833-958-37
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                           TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Common
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ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: O'Reilly, David
APPLICANT: Thomas, Christopher
TITLE OF INVENTION: IMPROVEMENTS RELATING TO THE
TITLE OF INVENTION: SPECIFICITY OF GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                       REGISTRATION NÚMBER: 30,742
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: GB 9
FILING DATE: 27-MAR 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER, GB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2319 base pairs
                                             FEATURE:
                                                                                                             ORIGINAL SOURCE:
                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2
                                                               STRAIN:
                                                                                       ORGANISM:
                                                                                                                                                    TOPOLOGY:
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    LOCATION:
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                            NAME/KEY:
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    Other
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                                                                                       Arabidopsis thaliana
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US-09-022-253-1
US-09-022-259-1
US-09-022-259-1
US-09-09-119-1
US-09-09-119-1
US-09-371-507-1
US-09-218-467B-1
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US-09-218-467B-1
US-09-218-467B-1
US-09-218-467B-2
US-09-08-186-650-2
US-09-08-186-650-2
US-09-08-186-650-2
US-09-08-187-453-31
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US-08-187-453-37
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US-08-222-177A-32
; Sequence 32, Application US/08222177A
: Patent No. 5582979
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; DATE: 1989
US-08-222-177A-27
                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                  APPLICANT: Weber, James L. TITLE OF INVENTION: LENGTH TITLE OF INVENTION: (dC-dA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: Weber, J. L.
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IDENTIFICATION METHOD: experime:
OTHER INFORMATION: /evidence= ie:
OTHER INFORMATION: /standard_nam
OTHER INFORMATION: /citation= ()
                                COUNTRY:
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AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS: Wasmuth, J. J. TITLE: Mapping of human TITLE: polymorphisms
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OTHER INFORMATION:
                                                           STATE:
                                                                          CITY: Madison
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IDENTIFICATION METHOD:
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                                                                                          STREET:
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                                                                                                        ADDRESSEE
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                            RY: USA
53717-1914
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                                                           Wisconsin
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Abundant Class of Human DNA Polymorphisms
Which Can Be/Typed Using the Polymerase Chain
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                                                                                       E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weber, James
                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kwitek, A. E.
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                                                                                                                                                 (dC-dA)n.(dG-dT)n SEQUE
                                                                                                                                                                                                                                                                                                                                                          1.7%; Score 23; DB
100.0%; Pred. No. 0.
tive 0; Mismatches
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/evidence= EXPERIMENTAL
/standard_name= "PCR primer"
/citation= ([1])
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/evidence= EXPERIMENTA
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/citation= ([2])
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H.
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                                                                                                                                                  SEQUENCES AND METHODS OF USING SAME
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0.057;
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                           DATE: 1990 PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            FEATURE:
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LENGTH: 240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                  PUBLICATION INFORMATION:
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NAME/KEY:
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                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                      LOCATION: complement (128..147)
IDENTIFICATION METHOD: experime
OTHER INFORMATION: /evidence- E
OTHER INFORMATION: /standard_na
OTHER INFORMATION: /citation- (
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IDENTIFICATION METHOD:
OTHER INFORMATION: /ev
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OTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
           AUTHORS: Weber, Jame AUTHORS: May, Paula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
                                                                          PAGES:
                                                                                                                          TITLE:
                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                              IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                   JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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EDNESS: double
                                                                                                                       Dinucleotide repeat polymorphism at the D15S87 locus
                                                                           4640-
                                                                                                                                                    Weber, J. L.
Kwitek, A. E.
May, P. E.
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                                                                                                        Nucleic Acids Res
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              , James L.
Paula E.
Class of Human
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/evidence= EXPERIMENTAL
/standard_name= "PCR pri
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_type= "tandem"
/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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/citation= ([1])
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FR: 09865.601
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DNA Polymorphisms
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                                                                                                                                                                                                                                                                                                                        "PCR primer"
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                                                                                                                                                                                                               "Only one strand sequenced"
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; PAGES: 388 ; DATE: 1989 US-08-222-177A-32

VOLUME:

388-396

JOURNAL:

Which Can Be Typed Using Reaction

the Polymerase Chain

Am. J. Hum. Genet.

Matches Query Match

23;

Conservative

Local

Similarity

1.7%; Score 23; 100.0%; Pred. No.

DB 1; 0.057; DB

Length 240

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                                                    Matches
                                                                              Query Match
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TELEX: 90-4030
INFORMATION FOR SEQ XD NO:
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                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 487 base pairs
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                          1227 GACACACACACACACACAAAT 1249
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MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                   NAME: MURASHIGE, KATE REGISTRATION NUMBER: 2
CACACACACACACACACAAAT 344
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WOLFF, ROGER K.
VENTION: METHOD TO DIAGNOSE HEREDITARY
                                                    Conservative
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Pred. No.
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RESULT 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NÓ: SEQUENCE CHARACTERISTÁCS:
                                                                                                                                                                                                                                                                                                    1227 CACACACACACACACACAAAT 1249
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FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                          CORRESPONDENCE ADDRESS:
                                                                     APPLICANT: WOLFF, I
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                              APPLICANT:
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                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                 FEDER, JOHN N.
GNIARE, ANDREAS
KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
WOLFF, ROGER K.
NVENTION: METHOD TO DIAGNOSE HI
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Pred. No.
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Copyright (c) 1993 - 2003
                                     /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/Backfiles1.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-049-475-5
US-09-734-675-3
US-09-739-913-1
US-08-618-745-12
US-08-650-598-1
US-08-620-598-1
US-08-620-598-1
US-08-620-6352-108
PCT-US96-06352-108
PCT-US96-06352-102
PCT-US96-06352-102
PCT-US96-06352-102
PCT-US96-06352-95
PCT-US96-06383-95
US-08-198-4468-9
US-08-837-953-37
US-08-837-8238-26
US-08-637-8238-26
US-08-637-8238-26
US-08-637-8238-26
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ALIGNMENTS

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Sequence 5, Application US/09049475 Patent No. 6140554
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FILING DATE: 27-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9706381.2
FILING DATE: 27-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                    NAME: COTUZZÍ, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 934
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2319 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: O'Reilly, David
APPLICANT: Thomas, Christopher
TITLE OF INVENTION: IMPROVEMENTS RELATING TO THE
TITLE OF INVENTION: SPECIFICITY OF GENE EXPRESSION
                                       FEATURE:
                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                      TELEFAX: (212, CONTROL OF TELEFAX: 66141 PENNIE
                                              STRAIN: Landsberg
                                                                       ORGANISM:
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                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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   LOCATION:
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1155 Avenue of the Americas
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PRIOR APPLICATION DATA:

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; LENGTH: 38844
; TYPE: DNA
; ORGANISM: Human
US-09-734-675-3
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Matches
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Patent No. 6365391
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
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Best Local :
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: AXYS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ISOLITITLE OF INVENTION: NUCL
TITLE OF INVENTION: USE:
FILE REFERENCE: CL000862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/734,675
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
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                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 CACACACACACACACACAAATAT 1251
                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              STREET: 285 mama
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LOCATION:
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OTHER INFORMATION: coding sequence- Arabidopsis
OTHER INFORMATION: apetala3 (GenBank ATHPETALA)
FILING DATE: 2
CLASSIFICATION:
                                                                                                    COMPUTER:
                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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                                                                                                                                                    94301
                                                                                                                                                                                     CA
                                                                                                                                                                                                                       E: Bozicevic & Reed, LLP
285 Hamilton Ave, Suite 200
                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ilarity 100.0%; I Conservative 0;
                                                                                               IBM Compatible
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               21-JAN-1998
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100.0%; Pred. No.
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(GenBank ATAGAMSG)
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0.0063;
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RESULT 4
US-08-118-200-12/c
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; MOLECULE TYPE: Genomic DNA
US-09-009-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.8%;
Best Local Similarity 100.0%;
Matches 25; Conservative
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                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LYNCH, Michael
TITLE OF INVENTION: DNA SEQUENCES RELATED TO ISOLATED
TITLE OF INVENTION: FRAGILE X SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                   APPLICATION NUMBER: US 0 FILING DATE: 20-MAR-1991
                                                                                                                                                             FILING DATE: 09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,677
                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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P.O. Box 1404
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MANDEL, Jean-Louis
PRITCHARD, Melanie April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAKER, Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAGARAJA,
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                                                                                                         US 07/802,650
US 07/638,518
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Pred. No. 0.0064;
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,745
FILING DATE: 02-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/118,200
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: US 07/802,650
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 020160-164
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                 APPLICATION NUMBER: FILING DATE: 20-MA
                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
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6242576
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MANDEL, Jean-Louis
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SCHLESSINGER, David
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                                 20-MAR-1991
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGILE X SYNDROME
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                                                 US 07/672,232
US 07/638,518

 Mismatches

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US-08-650-598-1/c
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; MOLECULE TYPE:
US-08-650-598-1
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                                                                                                                                                NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
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CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharo
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                   TELEFAX: 25-3856
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                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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TOPOLOGY: linear
                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marshall, O'Toole, Gerstein, Murray & Borun
00 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
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100.0%; Pred. No.
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Length 1611;

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RESULT 7
US-09-097-319A-1/c
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                                                                                                                                                                                                                                                                                                                    TELEFAX: 317 337 4847 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/097,319A
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NAME/KEY:
LOCATION:
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                                                                                                                                                            LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                             LOCATION:
                                                                                           NAME/KEY:
                                                                                                                    LOCATION:
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                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                          nucleic acid
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INVENTION: Regulatory Sequences for Transgenic Plants
F SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indiana
                                                                                                                                                                                                                                                                                                         6550 base pairs
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Hopkins, Nicole
Menke, Michael A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Kelley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petolino,
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4201..4425
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5383..5548
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5251..5382
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intron
5549..5649
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                                                                                                                                                                                                                                                       DNA
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100.0%; Pred. No.
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                                                                                                                                                                                                   /product= "Peroxidase"
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0.019;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
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                                                                                                          TISSUE TYPE: B
IMMEDIATE SOURCE:
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                                                  FEATURE:
                                                                              POSITION IN GENOME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
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STATE: Wiscon
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NAME/KEY: repeat_region LOCATION: 128..160 OTHER INFORMATION: /rpt.
                                                                                                                                         ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Ca
                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                      TELEX:
                                                                                                                                                                                                                                                                                                                  TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                  NAME: Sara, Charles S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                               CHROMOSOME/SEGMENT:
                                                                                                                                                                                                           TOPOLOGY:
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                                                                                             Mfd43
                                                                                                                                                                                                                                                     225 base pairs
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8000 Excelsior Drive, Suite 401
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..6068)
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5650..6065
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 /rpt_type= "tandem"
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                                                              59
                                                                                                                                            Caucasian
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0.019;
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US-08-222-177A-32
Sequence 32, Application US/08222177A
Pec. 10, 1996
SEMERAL INFORMATION:
APPLICANT: Weber, James L.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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AUTHORS:
AUTHORS:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymerase Chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS: McPherson, J. D.
AUTHORS: Wasmuth, J. J.
TITLE: Mapping of human chromosome 5 microsatellite
TITLE: polymorphisms
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OTHER INFORMATION:
                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 388-396
DATE: 1989
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                                                                                    CITY: Madison
                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL:
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IDENTIFICATION METHOD: experime
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                                                                  Wisconsin
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8000 Excelsior Drive, Suite 401
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/citation= ([1])
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/citation= ([1])
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/citation= ([2])
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/evidence= EXPERIMENTAL
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Pred. No. 0.057;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 225;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                    PUBLICATION INFORMATION:
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ORIGINAL SOURCE:
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APPLICATION NUMBER: US 0
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                       PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                        FEATURE:
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TISSUE TYPE: Blood
   AUTHORS:
TITLE: A
                                                                                                                                   AUTHORS: Weber, J. L.
AUTHORS: Kwitek, A. E.
AUTHORS: May, P. E.
TITLE: Dinucleotide repeat polymorphism at the
TITLE: D15S87 locus
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: complement (128..147)
LDENTIFICATION METHOD: experimes
OTHER INFORMATION: /evidence= E:
OTHER INFORMATION: /standard_name
OTHER INFORMATION: /citation= (
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LOCATION:
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OTHER INFORMATION:
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OTHER INFORMATION: /sta
                                                                   PAGES: 4640-
DATE: 1990
                                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                         NAME/KEY:
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                                                                                                        VOLUME:
                                                                                                                    JOURNAL:
                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
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                                  AUTHORS:
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: Weber, James L.
: May, Paula E.
Abundant Class of Human DNA Polymorphisms
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                                                                                                                     Nucleic
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SYSTEM: PC-DOS/MS-DOS
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/standard_name= "PCR primer"
/citation= ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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/evidence= EXPERIMENTAL
/standard_name= "PCR primer"
/citation= ([1])
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/evidence= EXPERIMENTAL
/standard_name= "Only or
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RESULT 11
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Best Local
                                                                                             Matches
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                                                                                                                       Query Match
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                                                                                                                                                                                                     TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 base pairs
                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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                                                                1227 CACACACACACACACACAAAT 1249
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY TITLE OF INVENTION: HEMOCHROMATOSIS
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COUNTRY: USA
TTD: 20006-1888
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                                      322 CACACACACACACACACAAAT 344
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VOLUME:
                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0: FILING DATE: 09-FEB-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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les 23; Conserv
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23; Conserv
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KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
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                                                                                            1.7%;
llarity 100.0%;
Conservative (
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Pred. No.
                                                                                                          Score 23;
Pred. No.
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                                                                                                         DB 1;
0.058;
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RESULT 12
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APPLICANT: FEDER, JOHN N.
APPLICANT: GNIRE, ANDREAS
APPLICANT: KIMMEL, BRUCE E
APPLICANT: THOMAS, WINSTON
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LENGTH: 487 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                         ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
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                                                                          TITLE OF INVENTION:
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                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                322 CACACACACACACACACAAAT 344
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TELEX: 90-4030
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                STREET:
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23; Conserv
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Washington
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                                                                         GNIRKE, ANDREAS
KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
NVENTION: METHOD TO DIAGNOSE HEREDITARY
NVENTION: HEMOCHROMATOSIS
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KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
NVENTION: METHOD TO DIAGNOSE HEREDITARY
            2000 Pennsylvania Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEDER,
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                                                                                                                                                                                     DRAYNA, DENNIS T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                              MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                         Score 23;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                              Mismatches
              N.W.,
                Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite 5500
                                                                                                                                                                                                                                                                                                                                                                             0.058;
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                                                                                                                                                                                                                                                                                                                                                                                          Length 487;
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COUNTRY:

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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/08599252 Patent No. 5705343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                        COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 487 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 90 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-FEB-
                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD TO DIAGNOTITLE OF INVENTION: HEMOCHROMATOSIS NUMBER OF SEQUENCES: 124
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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TELEFAX: (202) 887-0763
TELEX: 90-4030
                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                       APPLICATION NUMBER: US/08/599,252 FILING DATE: 09-FEB-1996
                                                                                                                                                                                                                                                                  STATE: DC
                                                                                                                                                                                                                                                                                    CITY: Washington
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                    ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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KIMMEL, BRUCE E.
THOMAS, WINSTON J.
WOLFF, ROGER K.
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PCT-US96-06352-102
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                                                                 PCT-US96-06352-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 102, Application PC/TUS9606352 GENERAL INFORMATION:
Query Match 1.7
Best Local Similarity 100.
Matches 23; Conservative
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                                                                                                                                                            INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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LENGTH: 672 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
APPLICATION UNBER: US 0.
FILING DATE: 09-FEB-1996
ATTORNEY/AGENT INFORMATION:
ANACE. WITERCHITCE PARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1500
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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LENGTH: 672 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                         TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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                                                                                                                                                                       TELEFAX: (202)
TELEX: 90-4030
                                                                                                                                                                                                                                   NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                           STRANDEDNESS:
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THOMAS, WINSTON J.
WOLFF, ROGER K.
VENTION: METHOD TO DIAGNOSE HEREDITARY
VENTION: HEMOCHROMATOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEDER, JOHN N.
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                                                                               linear
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1.7%; 5tt
100.0%; Pr
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   Score 23; DB 5; Length 672; pred. No. 0.059; Indels
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Gaps

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/599,252

FILING DATE: 09-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 9053-0001.21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

TELEPHONE: (202) 887-0763

TELEX: 90-4030

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 672 base pairs

TYPE: nucleic acid

STANDEDNESS: single

TOPOLOGY: linear

PCT-US96-06583-102
Search completed: January 18, 2003, 23:37:50 Job time: 198 secs
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PCT-US96-06583-102
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                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                    Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06583
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DRAYNA, DENNIS T.
APPLICANT: GNIRKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: HEMOCHROMATOSIS
NUMBER OF SEQUENCES: 124
                                                                                                           1227 CACACACACACACACACAAAT 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1227 CACACACACACACACACAAAT 1249
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CITY: Washington
STATE: DC
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ZIP: 20006-1888
                                                                                                                                                                    23;
                                                                                                                                                                  1.7%; Score 23; DB 5; Length 672; ilarity 100.0%; Pred. No. 0.059; Conservative 0; Mismatches 0; Indels
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Title:
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Maximum DB seq length: 2000000000
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2054640 seqs, 14551402878 residues
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gb_vi: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AF181722
Devuyst,O., Lorge,F., Weynants,P. and Boon,T. A new antigen recognized by cytolytic T lymphocytes on a human	Van Den Eynde, B.J., Gaugler, B., Probst-Kepper, M., Michaux, L.,	1 (bases 1 to 1382)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.		AF181722.1 GI:6684531	AF181722	Homo sapiens RU2AS (RU2) mRNA, complete cds.	AF181722 1382 bp mRNA linear PRI 10-JAN-2000	

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/db_xref="taxon:9606"
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VERSION KEYWORDS REFERENCE SOURCE ACCESSION ORGANISM Homo sapiens partial cds. AF181720 AF181720.1 G Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eukamania; Eutheria; Primates; Catarrhini; Hominidae; Homi Homo sapiens GI:6684526 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.

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Insert size: 117431; 9.3% error; agarose-fp
Quality coverage: 18.41x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
Chemistry: Dye-terminator ABI; 1% of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Consensus quality: 11824 bases at least Q40
Consensus quality: 118449 bases at least Q20
Consensus quality: 118634 bases at least Q20
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On Jun 12, 2001 this sequence version replaced g1:12331282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL132672.14 GI:14348905
HTG; HTGS_PHASE1; HTGS CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: dJ282H10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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mmalia; Eutheria; Primates;
(bases 1 to 120029)
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23430 23529: gap of 100 bp
23530 63600: contig of 40071 bp in length
63601 63700: gap of 100 bp
63701 100099: contig of 36399 bp in length
100100 100199: gap of 100 bp
100200 102366: contig of 2167 bp in length
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            CTGACGGCCCCAAAGGGTGCCTGAACGCCGCCGGTCACCTTCCAGGAAGACTTCGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGGTGGACAGCTTCTGAGCAGGAGCCGGAAACGCGCGGGGCCTTCAAACAGGCACGCC
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                                                                                                                      only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em: table, with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requests: clonerequest@sanger.ac.uk

On May 3, 2001 this sequence version replaced gi:13446455.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mappi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                 database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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Further information
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m clone RP11-95P3
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The true left end of clone RP11-95P3 is at 1 in this sequence. True left end of clone RP1-73M23 is at 152867 in this sequence. True right end of clone RP1-40E20 is at 17700 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-95P3 It may be shorter because we sequence overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr6
RP11-95P3 is from the library RPCI-11.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluSq repeat: matches 1. .311 of 3014. .3296 /note="match: STS: Em:G27290" 3014. .3093 /note="40 copies 2 mer ga 75% conserved" 5024. .5477
                                                                                                                                                                                                                                                                         complement(9393. .9853)
/note="match: GSS: Em:AQ285817"
10311 .10437
/note="L2 repeat: matches 2612.
10710 .11022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="FLAM_C repeat: matches 1.
6971. .7198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="LIMEc repeat: matches 2228. .2259 of consensus"
6367. .6515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSg repeat: matches 18. .294 of consensus"
5986. .6359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Alusx repeat: matches 1..303 of consensus" 1327. 1448 /note="Aluso/FRAM repeat: matches 181..298 of con: 2264. 2575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 65. .262 of consensus" 521. .582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=1
                                                                          /note="38 copies 4
13785. .14820
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32. .494
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19. .544
/note="L1PB3 repeat: matches 5106. .6149 of consensus"
16029. .16110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2683.
720. .1022
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/chromosome="6"
                                                                                                                      /note="114 copies 2
13479. .13630
                                                                                                                                                                                                                                    /note="AluJo repeat: matches 1.
12006. .12156
                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:B54691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="L2 repeat: matches 1512.
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                                                                                                                                                                            note="L2 repeat: matches 1374.
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                                         .16008
                                                                                                                                                                                               L2 repeat: matches 2594.
.13011
                                                     repeat: matches 4766. .5798 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                       .445 of
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complement(19065. 19495)
/note="match: GSS: Em:AQ545892"
complement(19130. 19546)
/note="match: GSS: Em:B94529"
19265. 19495
                                                                                                                                                                                                                                                                           23980. .24292

//note="Alusq repeat: matches 2.complement(27208. .27677)

complement(27208. .27677)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS: Em:AQ268095"
complement(19370. .19546)
/note="match: GSS: Em:AQ128461"
                                                                                                 complement(30720. .31207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(19269. .19546)
/note="match: GSS: Em:AQ663911"
complement(19325. .19546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MER4D repeat:
complement(18929. .1)
                                                                           /note="match: STS: 30919. .31120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="match: GSS: Em:AQ021494"
complement(19337. .19501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement
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16428. 16829
/note="L1MC3 repeat: matches
16868. .17150
                                                    /note="MER58A repeat: 32109. .32472
                                                                                                                                                                                                                                                                                                                                                                                                                    /note="70 copies 2 mer aa 60% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match: GSS:
natch: STS: Em:G592
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complement(19031. .19542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="MER67C repeat:
18676. .18729
                                                                                                                                                                 /note="L2 repeat: matches 2323.
                                                                                                                                                                                         /note="MLT1H repeat: matches 433.
                                                                                                                                                                                                                                          note="AluJb repeat: matches 163.
                                                                                                                                                                                                                                                                   note="match: GSS:
                                                                                                                                                                                                                                                                                                                                              note="AluJb repeat: matches 4.
                                                                                                                                                                                                                                                                                                                                                                      note="19 copies 4
                                                                                                                                                                                                                                                                                                                                                                                            /note="20 copies 4 mer aaag 80% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note≖"AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSg/x repeat: matches 126.
19740. .20100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MD3
mik repeat: matches .34331
                                                                                                                             .30547
                                                                                                                                                       .29834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .19739
                                                                                                                                                                                                                                                                                                                                                                                                            .22670
                                                                                                                                                                                                                                                                                                          L2 repeat: matches 2580.
.24292
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Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hasiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
                                                                         cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                             Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 1287)
                                                                                                                                                                                                                                                                                                                                          Homo sapiens, clone MGC:22980
BC014954
BC014954.1 GI:15928979
                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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 GACGGGCTGAGACAGGTGGCTGGACCTGGCGCGTGCTGCCGCGCTCATCTTCCCCGCTGGCCG
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                                                                                           AACGCCGCCGGTCACCTTCCAGGAAGACTTCGAAGCTGGACACCTTCTTCTCATGGAT
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Conservative

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Mismatches

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863 733 803 793 853 683 913 623 973 563 1093 443 1153 49.38; 100.08;

Score 682; Pred. No.

0 DΒ

9; 0,

Length

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Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLML at: http://image.lln Series: IRAL Plate: 34 Row: m Column: 13 This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schein, Duane Smailus, Michael Smith, Lorraine Spence, Michael Thorne, Miranada Tsai, Natasja van den Bosch, George Yang, Scott Zuyderduyn, Marco Marra.
343
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/lab_host="DH10B-R"
  Ø
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                                                                                                                                                                                                                                                                          /note="Vector: 181. .984
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                                          TCTAGCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGTAGATGTTCCTGACGGCCCCAAAG 675
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                       TCTAGCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGTAGATGTTCCTGACGGCCCCAAAG
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Direct Submission
Submitted (30-AUG-1999) Ludwig Institute for Cancer Research,
Avenue Hippocrate, 74, Brussels 1200, Belgium
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van Den Eynde, B.J., Gaugler, B., Probst-Kepper, M., Michaux, L., Devuyst, O., Lorge, F., Weynants, P. and Boon, T. A new antigen recognized by cytolytic T lymphocytes on a human kidney tumor results from reverse strand transcription
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Mammalia; Eutheria;
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                                                                                                                                                                      Conservative
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DHSEQGARPARVNGGTPEENGEELQQVNNELQLVLDKERKSQGAGSGQDEADVDPQRP
PRPEVKITSPEENENNQQNKDYAAVA"
75 a 440 c 576 g 476 t
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                                                                                                                                                                                                                    Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                               2 (bases 1 to 2003)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
                                                                                                                           NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                           Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence). Homo sapiens hepatoma cell_line:HepG2 cDNA
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Homo sapiens cDNA: FLJ23383 fis,
AF181721 Homo sapiens RU2S mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                            NEDO human cDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK027036.1 GI:10440050
                                                                                                            University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (sites)
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP16466"
                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
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                                                                                                                                                                                                                                                  AUTHORS
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Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research In Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
On May 9, 2002 this sequence version replaced gi:6330108. 1. .6548
                                                                                                              2 (bases 1 to 6548)
Ohara,O., Nagase,T. and
Direct Submission
                                                                                                                                                                           from size-fractionated cDNA libraries from human DNA Res. 6 (5), 329-336 (1999) 20039618
                                                                                                                                                                                                                      Characterization of cDNA clones selected by
                                                                                                                                                                                                                                                  Hirosawa, M., Nagase, T.,
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                       Homo sapiens adult male brain cDNA to mRNA, clone_lib:pBluescriptII SK plus clone:hh03679s1.
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/clone_lib="HEP"
/note="cloning vector
1. .2003
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                                                                                                                                                                                                                                                                              Eutheria;
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Pred. No. 1.5e-204;
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                                                                                                                               Kikuno, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293;
AL359683.4 GI:15487186
C3HC4 zinc-finger protein; DEAD-box helicase; DNA polymerase I, thermostable; exonuclease; flagellar radial spoke protein; quanosine diphosphatase; long-chain-fatty-acid-coa ligase; mcak-related kinesin; mitogen-activated protein kinase; MORN-domain protein; n-acetyltransferase subunit; nucleolar protein involved in pre-rRNA; PDZ-domain protein; protein kinase a regulatory subunit; ras-related protein; surfeit l-related protein; thermostable carboxypeptidase l; trab5b; tubulin alpha chain; y42g9a.3 protein. Leishmania major.
                                                                                                                                                                                                                                                          Leishmania major
AL359683
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KGKKEDVNSEKLTKLKQNVKLKNSQETI PNSDBGIFRAGAERSETGAAEVQEDEDTQ
VEVPVDQRPAEIJDEEDGEKANKDAEQKEDFSGMNGDLEEEGGREATDAPEQVEEIL
DHSEQQARPARVNGGTDEENGEELQQVNNELQLYLDKERKSQGAGSGQDEADVDPQRP
PRPEVKITSPEENENNQQNKDYAAVA*
1124 c 1377 g 1967 t
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GEIKKRPMEVVNTEVKPVIHSRINVSARFKRLDEFCTIFLIANGDLINGFYVAVGRDKFKKL
KTLNQWDHVLQMVTEKITLRSGAVHRLYTLEGKLVESGAELENGQFYVAVGRDKFKKL
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/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
/note="This sequence was obtained by subcloning of the DNA
/note="This sequence was obtained by subcloning of the DNA
/ragments derived from two cDNA clones (1 - 1251 was
derived from a RT-PCR product (Kidney) and 1252 - 6548 was
derived from hh03679)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="KIAA1154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"hh03679s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "KIAA1154"
                                                                                                                                                                                                                                                                                 Friedlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 293; DB 9; L
Pred. No. 3.8e-164;
                                                                                                                                                                                                                                                                                                       221641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                 chromosome 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                    PAC
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                                                                                                                                                                                                                                                                                 linear
C P1046.
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                                                                                                                                            MORN-domain
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PUBMED
gene
                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                  sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmids L2802 (AL359774) and L6293 (AL359777) are contained in PAC P1046. PAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 see http://www.sanger.ac.uk/Projects/L_major/
CDS are numbered using the following system eg P1046.01. P1046 (PAC name), .01 (first CDS)
To make the PAC library Leishmania major Friedlin DNA was partially digested with NotI prior to cloning into the NotI site of the PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, (E-mail: barrell@sanger.ac. and Katholieke Universiteit Leuven, Faculty of Agricultural and Applied Biological Sciences, Department of Animal Production, Laboratory of Gene Technology, Willem de Croylaan 42 on Sep 6, 2001 this sequence version replaced g1:13159932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the sto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon. Transmembrane domains were predicted as implemented at the TMHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.kazusa.or.jp/codon/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon preference based on the codon usage table for Leishmania at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the FramePlot program of Bibb et al., Gene 30:157-166(1984) as implemented
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene prediction is done using:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector PCYPAC2N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of leishmania sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see http://www.ebi.ac.uk/parasites/leish.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-SEP-2001) European Leishmania major Friedlin genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 221641)
Aert,R., Robben,J., Volckaert,G., Ivens,A.C., Quail,M.,
Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ivens, A.C., Lewis, S.M., Bagherzadeh, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 221641)
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                                                                                                                                                                                                                                                               overlapped by cosmid L7913 (AL603794). Location/Qualifiers
                               /clone="PAC P1046"
                                                                          /db_xref="taxon:5664"
/chromosome="13"
                                                                                                                                                 /organism="Leishmania major"
/strain="Friedlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                    .221641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (E-mail: barrell@sanger.ac.uk)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang, L., Chan, H.M.
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/note-"P1046.02, predicted protein, len = 1428 aa, possibly DNA polymerase I, thermostable; predicted pI = 8.3748; contains Pfam match to entry PF00476 DNA_pol_A; contains match to PROSITE PS00447 DNA polymerase family A signature; contains Pfam match to entry PF00929 Exonuclease; contains Pfam match to entry PF00929 Exonuclease; contains no predicted TM helices; reasonable similarity to DPOI_THEAQ, DNA polymerase I, thermostable (EC 2.7.7.7) (832 aa, Thermus aquaticus, EMBL: D32013, BAA06775); Fasta scores: E():6.9e-07, 28.045% identity (32.143% ungapped) in 353 aa overlap, (aa 1021-1366 of D1046, 02, aa 515-829 of DPOI_THEAQ)"
                                                                                                                                 VVYYASEVSERLIGCYGSDLMRYWGAMKETASFIDADLLFGIYTAAGNTLRSYQRKKL
SQSHTCDHLSILNSSDEGIATPQNALMWACYETLPRRVAAEKAELRHYDKFITIAYVS
TDHTVHAQPVNPVADINHVLSACITDHAVWACYETLPRRVAAEKAELRHYDKFITIAYVS
TDHTVHAQPVNPVADINHVLSACITDHAVROVTLAEYLLAACTTGSNSLHDLAALRHGVQV
DAKSLVILLGSQDAELQKFIKRGGRVWCVTLAEYLLBAQRCTTGSNSLHDLAALRHGVDL
PPSSRYGTPNIRLFFALQRQFILHAAAFAVVKVEVEQLKRALEQCQVLSLAHRWDSLLA
MTSIEKAGIHIDAEEAARQTASIKSAACAVVKVEVEQLKRALEQCQVLSLAHRWDSLLA
HAYFFGTISLGHQAYARDTPLWTSNVVHLCHRYGAFLHWVGELHLQRYAACALPTS
                                                                                                                                                                                                                                                                                                                                                                                                     /note="P1046.01, predicted protein, len > 408 aa, unknown; predicted pI = 10.6399; contains no predicted TM helices; some similarity to APE_CANFA, apolipoprotein e (305 aa, Canis familiaris, EMBL:); Fasta scores: E():0.59, 27.8798 identity (29.677% ungapped) in 165 aa overlap, (aa 12-173 of P1046.01, aa 84-241 of APE_CANFA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="possible DNA polymerase I, thermostable"
/protein_id="CAC37107.1"
/db_xref="GI:13751093"
VFSVDEPMLRRALECHAPECQLDGILFCDSLALLNAHRSELRWRMRTKRTNQPLMDAL
ASSLRLSRLITALNVRPEGDLHRADTDTKALMYVLINILGVADKDAVAQRDKILIEAA
                                                                            GGLPSRIHQHIEVQGSQKLKTYRVVFFDIETTGLNPSTDAIVEVAMFDPIENSTFHTL
VNPQRPITPRTVGIHHITNAMVRDAPTVDVVAKSIGQYLRLDKASYNPHEILVLVGHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(3457. .7746)
/gene="P1046.02"
/note="P1046.02, predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="poly-pyrimidine tract"
complement(2790. .2805)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRVEGHLEEKRQQEVARFSFRPTISARARTMQSSRPVVERLYSGTADAGTDTATFTDV
TNLRSSSGEKTKTASMATYQRLYQDAVTRRAHDQMQEKLARVRSKNEFCPCTDSVSGL
IASKRGDTTRERLLRPKAALDVARDVYPQETFAPRINTSTRFERVPLSARAAIMQRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(3457
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complement(1820. .1837)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="poly-pyrimidine tract"
complement(1757. .1771)
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complement(1729. .1743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1293. .1311)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q9BHX9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P1046.02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRRVDLEASAPLPESGR"
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/db_xref="GI:15487187"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="poly-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q9BHY0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=:
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PUBMED
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AUTHORS
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SOURCE
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AC024857/c
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                                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda;
Rhabditoidea; Rhabditidae; Pel
Harmon,G., Lamar,B., Du,H.
The sequence of C. elegans
Unpublished (2001)
3 (bases 1 to 38967)
                                                                                                                            Genome sequence of the nematode C. elegans: investigating biology. The C. elegans Sequent Science 282 (5396), 2012-2018 (1998)
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AC024857.2 GI:20198913
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(bases 1 to 38967)
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8143. .8160
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DFHVKRAAFFSGLPYDEIYQGYKRNVPKYVKLBRTAKQFSFQRLYGAGYVPLLHKTTGI
PVKDLEAS IQRENEEYPGIAQFHRI IRSVALBRUNDGLPTSFIAEMPTGLRMSLRTBO
VVLNLFPIKNYFPIQGYGAELAQMMLGRLYRHFYRKDFYDDRAFLINFVBDSVMMDCHV
DVLRECVRDTCRILGSVHEYVPKVFPGVKISVPLQVSASCGVDMCSMESIKGDDYMFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="poly-pyrimidine tract"
complement(10073. .10108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="poly-pyrimidine tract" complement(9472. .9487) /note="poly-pyrimidine tract" complement(9851. .9866)
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8288. .8303
/note="poly-pyrimidine tract"
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/gene="P1046.02"
/note="Pfam match to entry PF00929 Exonuclease,
Exonuclease, score 63.00, E-value 6.5e-15"
5600 C1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match to PROSITE PS00447 DNA polymerase family A signature"
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complement(9357. .9373)
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complement(9311. .9341)
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complement(9244. .9263)
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complement(8882. .8898)
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/gene="P1046.02"
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                                                       and Wohldmann, P
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d Y71G12A,
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Sequencing Consortium
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E-value 9.6e-08
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Direct Submission
Submitted (23-JUN-2001) Department of Genetics, Washington
Submitted (23-JUN-2001) Center, 4444 Forest Park Avenue,
                                                                                                                                  University, Genome Sequencing Center,
Louis, MO 63110, USA
On Apr 19, 2002 this sequence version
                                                                                                                                                                                                                                                                   Submitted (12-FEB-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-NOV-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue, Louis, MO 63110, USA
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Submitted (Ol-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                      Submitted by:
                                                                                                                                                                        Submitted (19-APR-2002) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Ave
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Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                         Department of Genetics, Wasi
St. Louis , MO 63110, USA,
                                                                                                Genome Sequencing Center
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Park Avenue, St. Louis,
                                                                                 Washington University
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Missouri 63108,
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neighboring submissions. NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from than one m13 subclone.

For a graphical representation of this cosmid sequence and its (www.wormbase.org/db/seq/sequence?name=Y71G12A;class=Sequence)

NEIGHBORING COSMID INFORMATION

The 5' cosmid is M01D7, overlap. 3500 đđ overlap; the ω cosmid is Y51F10,

Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORTEOME (aloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses

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FEATURES
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EIVTVDLWKMMGCSSKKVDKLPIPLKEWNALRELDHFVIRCRIPAGDMCSYVCSVVD
ARCYCTIRPLARGSHTYLGFEHLGGLVPLLLGRQVNRFLDGFQIFMYQSKPPTSSP
GGSSAQVEDVNSIFKKTYLGFEHLGGLVPLLLMSRHVRPTREDTRLLQVTSNVWCT
RFNISSLSPSLLPTFLGQVIYKTSVLHLQPRQMTIDLAVLQRKDGKELPEASVDGTTH
MTSSPDQGLTSEERQFFQKILAECLSLRAVINSSNFGKPPPPAAASTISLPCQPSTSK
                           join(21672. .21741,21793. .21874,21935. .22133,22912. .23214,
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/gene="Y71G12A.2"
                                                                                                                              /gene="Y71612A.2"
/gene="Y71612A.2"
/note="for a graphical representation of this gene see:
[www.wormbase.org/db/seq/sequence?name=Y71612A.2;class=Seq
                                                                                                                                                                                                                                                                                                    WFDMFPSLEKSKGIGSPTLICHGEKDYIVGHEHGVLLKDTIPDCELHLLQHASHQGIF
CEREMWDRVEAFLGSRVGITRNWIEHLQSETSISVVPDFCSSSQVISMSRETAEHFRA
                                                                                                                                                                                                                                                                                                                                                            PPYPPKLFRKIVFCSPQKGRYYYLIAAKGTKRKACFQASEADGYEHLSISLPQMIKPK
VRAIDVFYHLLRCKVFTLPYDEKHKICAMELYCEGSIRWIHRDKNRQRLRSPNLIIFS
QPNSSDLGCCLMMDPNFADIADFLQCDLLIVDYPGYGVSEGTTNEKNVYAAVBAVNKY
AMGTLGYSQDKIILIGFSLGTAAMVHVAEMYKVAAVVLIAPFTSFFRIVCRRPSIIRP
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19078. .19309,20134. .20422,21106. .21181,21275. .21300))
/gene="Y71G12A.4"
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/gene="Y71G12A.4"
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TGWAAMEQASKKDAEVIRSHVDKLASIAEQLSKRHGDFNVKRDKASINKMRSQMKTLL
RRVNEIEQKVANGDVKTEVRQLLNTLNEMKKALGEGVPKSGRSLNSTCKIETMINKTP
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VWAPDSRQLVLGFSTGTIQVLSNAGVNITSRSFTEDKLTQMAFSPLRTKVREVEWTLA
MLSSANKIYMISAYDQLHPAIYRSKFQVIRMEWNTDGTILALINANNELVMIDTTCRV
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GVTLTDFKPTPDDLTRYNFNLRGHHNAIRMVTWNKSQSKLASCDASGIIYVWVRNDDR
                                                                                                                                                                                                                                                                     KTRDLEQQQSNCH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein Y71G12A.4"
/protein_id="AAK31567.2"
/db.xref="G1:18652638"
/translation="MRNFKRGAKKERKTAGLCTELHLSVATGPNGENTMSATLAPEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="coded for by the following C. elegans cDNAs: yk607e5.3, yk607e5.5"
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/protein_id="AAK31566.2"
/db_xref="GI:20198914"
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8366. .8671,9772. .9909)
/gene="Y71G12A.3"
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \mathtt{ATIVSNLQSAVCLNVAHRVACPAHDSKLWSDVMQKSFSIWKIISRILLIIVSIFFVLL}
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[www.wormbase.org/db/seq/sequence?name=Y71G12A.4;class=Seq
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'note="similar to pir||I38919 probable transmembrane
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Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditida; Chromadorea; Rhabditida;
Eukaryota; Metazoa; Nematoda; Chromadorea; Caenorhabditis.
                                                                                   Direct Submission
Submitted (11-OCT-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                           University, Genome Sequencing Center, 4444 Forest Park Avenue, St. Louis, MO 63110, USA 5 (bases 1 to 41179)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Caenorhabditis elegans cosmid M01D7, complete sequence.
AF003739
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                                                                                                                                                        Waterston, R.
                                                                                                                                                                                                                                                 Submitted (09-AUG-2001) Department of Genetics, Washington
                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of C. elegans
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LHLARDALFVLAKQLKINPEDSETLGKWLLSIKPISLESKVLSSAIKSNEQMCTEME
KVHDVCVGSLMHANNHREFVWNITYKLENYLRSSNSKCPLQKLSINRQMKTELPTQAST
AQMLKSLCSELLESDSTTDEMLTLIFFIVQCENGKDEKIVENLMEKMRKRAEIDGKLV
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TEYARLYWSFGAIEYAMSIFDDLEKLLHEFVLRSGEPESPKWLAQLLNTKIDDRPTLI
SGGFSVQRISKSEAHYLGMRNYLLCQQIIMSIHLYQQKMKSNDAAPSLRSDCAVGIMQ
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for by the following C. elegans cDNAs: yk47c9.5,
yk191g7.5, yk270h3.5, yk346a2.5, yk406g2.5, yk853b04.5
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/protein_id="AAK31568.4"
/db_xref="G1:18652637"
/translation="MDRDLLDINGLSKSFQKNSVIISHAGVDQSFSVYQHALVSYFSR
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Submitted (19-APR-2002) Department of Genetics, Washington

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.ddbj.nig.ac.jp/c-elegans/html/CE_INDEX.html) and The C. elegans ORFecome cloning project (http://worfdb.dfci.harvard.edu/), similarity to other proteins from BlastX analyses (http://blast.wustl.edu/), sequence conservation with C. briggsae using Jim Kent's WABA alignment program (Genome Research 10:1115-1125, 2000), individual C. elegans GenBank submissions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were double stranded, sequenced with an alternate chemis or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence in the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not be the entire insert of this close it may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and personal communications with C. elegans researchers. tRI are predicted using the program tRNAscan-SE (Lowe, T.M. and Eddy, S.R., 1997, Nucl. Acids. Res., 25, 955-964).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coding seqences below are the result of integration and manual review of the following data: computer analysis using the program Genefinder (P. Green and L. Hillier, personal communication), the large scale EST projects of Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neighboring submissions
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On Aug 9, 2001 t
Submitted by:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
(GB:U56864); contains similarity to Pram usuality (GB:U56864); contains similarity to Pram usuality (GB:U56864); contains similarity to Pram usuality (GB:U56864); contains similarity to Pram usuality (GB:U56864); coded for by the following C. elegans cDNAs: yk290g12.5, yk392d2.5; yk392d2.5; yk377b4.5; yk34966.5; yk46266.5; yk343g12.5; yk343g12.5; yk413b9.5; yk272f9.5; yk343g12.3; yk628a12.5; yk343g12.5; yk413b9.5; yk529e9.5; yk53f121.5; yk63c6.5; yk63c6.3; yk681e8.3; yk587a10.5; yk681a11.5; yk622a12.3; yk654c6.3; yk681e8.3; yk587a10.5; yk681a11.5; yk622a12.3; yk634c6.3; yk681e8.3; yk587a10.5; yk681a11.5; yk622a12.3; yk684c6.3; yk681e8.3;
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4211. .43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="egl-30"
/note="for a graphical representation of this gene see:
/www.wormbase.org/db/seq/sequence?name=M01D7.7a;class=Sequ
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/db_xref="taxon:6239"
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alternatively-spliced form; coded for by the following
elegans cDNAs: yk514a3.5"
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GKSTFIKQMRIHGGGYSEEDKRAHIRLVYQNVFMAIQSMIRAMDTLDIKFGNESEEL
QEKAAVVREVPDESVTSFEEPYVSYIKELWEDSGIQECVDRRREYQLTDSAKYYLSDL
RRLAVEDYLPFEQDILRVRVPFTGIIEYPFDLEQIIFRWDVGGQRSERKWHHGFEN
VTSIMFLVALSEYDQVLVECDNENRMEESKALFRTIITYPWFTNSSVILFLNKKDLLE
                                                 pun(/523. .7577,7657. .7715,7773. .7901)
/gene="nlp-12"
/note-"c
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein M01D7.6"
/product="Hypothetical protein M01D7.6"
/protein id="AAB58065.1"
/protein id="AAB58065.1"
/db_xref="GI:2105483"
/translation="MDYSQLTDAELRDSLKSHGVSVGPIVATTRKLYEKKLIKLSDGS
/translation="MDYSQLTDAELRDSLKSHGVSVGPIVATTAAATTSPESDSDDCEESMR
INNQSNLNDSQFNEDSLIISSSPKKSPPQRVFQNVSAATAAATTSPESDSDDCEESMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for by the following C. elegans cDNAs: yk79h4.5, yk113e10.5, yk113e10.3, yk79h4.3, yk142h6.3, yk142h6.5, yk196b5.5, yk28d11.3, yk258d11.5, yk466f7.5, yk589h7.5, yk668d10.5, yk669g2.5, yk669g2.3, yk668d10.3, yk589h7.3*
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KKDLLEEKILYSHLADYFPEYDGPPRDPIAAREFILKMFVDLNPDADKIIYSHFTCAT
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YYLSDLRRLAVPDYLPTEQDILRVRVPTTGIIEYPFDLEQIIFRWYDVGGQRSERRKW
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sequence M01D7.7b)"
/protein_id="AAM15593.1"
/db_xref="GI:20198865"
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/gene="MO1D7.8"
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sequence M01D7.7a)
                                                                                                                                                                                               /gene="nlp-12"
/note="for a graphical representation of this gene see:
{www.wormbase.org/db/seg/sequence?name=MOlD7.5;class=Seque
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/gene-"MO1D7.6"
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/protein_id="AAM15594.1"
/db_xreff="GI:20198866"
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/db_xref="GI:2105489"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="for a graphical representation of this
{www.wormbase.org/db/seq/sequence?name-M01D7.(
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4211. .4364,4435. .454
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|www.wormbase.org/db/seq/sequence?name=M01D7.8;class=Seque
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4542,4922. .500
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                                                                                                                                                                                                                                              Submitted (22-NOV-2001) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
The control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                            Center code: WIBR
                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
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/protein_id="AAB58066.1"
/db_xref="GI:2105484"
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YRPLQFGKRDYRPLQFGKRSSGSSGPVVLEPIWEWQ"
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/product="C. elegans NLP-12 protein (corresponding
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                                                                                                                                                                                                                   Genome Center
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Pred. No. 4.3e-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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REFERENCE

JOURNAL AUTHORS

TITLE AUTHORS

REFERENCE

COMMENT

JOURNAL

RESULT 12 AC100574

Qy

Matches

gene

LOCUS

VERSION

KEYWORDS

SOURCE

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Center project name: L15715
Center clone name: 155_0_10
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NOTE: This record contains 62 individual

sequencing reads that have not been sequencing reads that have not been sequencing. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone that the sevent that

be the record is updated, the accession number will 10406 11114: contry of the control of th preserved. 20006 20106 16775 16874: gap of 16875 17545: con 9612 1030 10306 10405: 20828 18342 18441: 17546 17645: 17646 183 15974 16073: 14352 14451: 16074 1495 1594: gap of 1595 2314: co 9512 9611: 4680 4779: gap of 4780 5453: cor 3902 4001: 682 781: 782 1 7066 7165: 100 bp 100 8005: gap of 100 bp 100 bp 1710: contig of 705 bp 11 8810: gap of 100 bn 1 9511: contic 2314: contig of 7 15 2414: gap of 100 5 3097: contig <2 0 8 3107 5453: contig of 674 k 5553: gap of 100 bp 6250: contig of 697 k 15253: 22536: 21722: 20927: 20105: 19266: 3197: 23336: 18341: cr July 1 18341: cr July 1 1441: cr July 1 .8441: gap of 100 bp 19166; contig of 725 bp 1 9266; gap of 100 bp 20005; contig of 739 bp 1 0105; gap of 100 bp 105; gap of 100 bp 1027; gap of 100 bp 10927; gap of 100 bp 10027; gap of 1002 100 bp
100 bp
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10 u: contig of 6 1494: cor. 21622: contig of 695 1 1721: gap of 100 bj 22436: contig of 714 1 2536: gap of 100 bj 23236: contig of 700 j ;: contig c ;: gap of 3901: cc 1: ar 10305: contig of 694 by 405: gap of 100 bp 111114: contig of 700 24029: c 15973: contig of 720 bp 173: gap of 100 bp 16774: contig of 701 bp 15973: cont 529: gap of 100 bp 14351: contig of 722 bp 151: gap of 100 bp 15153: contig of 702 bp 100 k
3311: contig of 701
: gap of 171
7305 contig of 696 bp of 100 bp contig of 678 b of 100 bp contig of 713 bp in of 683 100 720 100 bp of 671 bp 100 bp 100 bp of 674 k 100 bp 100 100 bp 100 bp 100 bp 681 bp in length þ þ ď bp in đđ bp in đđ bp in bp in bp in bp in bp in bp in length đq dq bp in 'n in in 'n 'n in 'n 'n 'n in in 'n ίn 'n ij in ij 'n in length
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BASE COUNT
ORIGIN
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                                                                                    source
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45795 464
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45021 456
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40162 40261: gap of 100 bp
40262 40927: contig of 666 bp in length
40928 41027: gap of 100 bp
41028 41708: contig of 681 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6054 36153:
      /organism="Mus musculus"
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/db_oref="taxon:10090"
/clone="RP23-155010"
/clone_lib="RPCI-23 Female Mouse BAC"
/clone_lib="RPCI-23 Female Mouse BAC"
/clone_lib="RPCI-23 Female Mouse BAC"
                                                                                             0 49009: gap of 100 l
0 49743: contig of 734
Location/Qualifiers
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42495: ~
595.
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3211: contig of 697 bp
1211: gap of 100 bp
100 bp
32905: contig of 694 bp
1005: gap of 100 bp
33703: contig of 698 bp
                                                                                                                                                                                               994: gap of 100 bp
46495: contig of 702 bp in length
596: gap of 100 bp
47305: contig of 709 bp in length
                                                                                                                                                                                                                                                                                  395: gap of 100 bp
43278: contig of 683 bp in length
378: gap of 100 bp
44113: contig of 735 bp in length
213: gap of 100 bp
214920: contig of 707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31314: contig of 721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771: gap of 100 bp 30493: contig of 722 bp
                                                                                                                                         48909: contig of 719
                                                                                                                                                                      48090: contig of 685
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25610: contig of 694 bp in length
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24816: contig
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27268: contig of 721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10: gap of 100 bp
26447: contig of 737 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58: gap of 100 m
28071: contig of 703
                                                                                                                                                                                                                                                          100 bp 100 bp 5694: contig of 674 bp
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16053: contig of 684 bp in length
33: gap of 100 bp
6884: contig of 731 bp in length
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contig of 715 bp
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of 687 bp
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100 bp in )
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f 720 bp in length
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Sequence split into 5 fragments I
Fragment Name Begin En
AC079517_1 100001 21
AC079517_2 200001 31
AC079517_3 300001 41
AC079517_4 400001 41
Continuation (4 of 5) of AC079517 fi
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AUTHORS
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VERSION
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AC097411/c
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AC079517_3/c
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Homsif, Howard,S., Hubber,J., HulyK,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Lozado,R.J., Lu,X., Lucier,A., Martindale,A., Martinez,E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Brya Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C. Carker, F., Carter, M., Cavazos, S.R., Chacko, J., Chavez Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Davi Davila, M.L., Davis, C., Davy-Carroll, L., Davier, C., Davy-Carroll, L., Davis, C., Davy-Carroll, L., Davis, C., Davy-Carroll, L., Davis, C., Davy-Carroll, C.
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Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Earnhart,C., Edgar,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Erantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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|6, *** SEQUENCING
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Direct Submission
Submitted (18-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (base 1 to 119318)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 11, 2002 this sequence version replaced gi:17973555.
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Center clone name: CH230-142N16
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Chemistry: Dye-terminator Big Dye: 100% of rea
Assembly program: Phrap; version 0.990329
Consensus quality: 5851 bases at least Q40
Consensus quality: 62883 bases at least Q30
Consensus quality: 66623 bases at least Q20
                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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Submitted (20-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 20, 2001 this sequence version replaced gi:14550304.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                  www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.3% of Sequence;
Estimated Total Number of Errors is 0.5.
                                                                                                                                                                                                                                                                                                                                                            Submitted (26-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 139846)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CONA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2558 row: e column: 01
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:6376296"
/clone_lib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="PH10B (phage-resistant)"
/lab_host="PH10B (phage-resistant)"
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Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert St
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National Institutes of Health, Mammalian
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/tlosue_type="normal pigmented retinal epithelium"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Organ: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Corgan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Corgan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/note="Corgan: eye; Vector: poTB7; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5;
/cloned int
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/db_xref="taxon:9606"
/clone="IMAGE:6376418"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLCMA2487 row: g column: 06 High quality sequence stop: 667.
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1 (bases 1 to 898)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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/tlab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by Oigo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                     Library.
a 252
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/clone="IMAGE:6286493"
/clone_lib="NIH_MGC_100"
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E 1 (bases 1 to 963)

E NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: CGAP (Stanford)

Tissue Procurement: CGAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
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                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
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                                               quality sequence stop:
Location/Qualifiers
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/db_xref="taxon:9606"
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BM833169
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Kim, Y.S.
                                    Kim, N.S.,
                                                                                 Mammalia;
                                                                                                                  Homo sapiens
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/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: liver; Vector: pOPB7; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: pOPB7; Site_1: XhoI; Site_2:
/note="CONA made by oligo-df priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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a 350
                              Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 to 486)

Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
                                                                                                                                                                                  GI:19189578
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Primates;
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Pred. No.
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                      Park, H.S.,
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S5SNU484s1-12-C04
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                      Kim, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                             470
                                                                                                                                                                                                                                                                                                                                                                                   264 TITGGTCACTAACCTTTGCAAGGATACCTTTTTATTTCTTTAAGATTCCTGTTGTTTAT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
CCCCACACTATAGGGCACCTAAATGGGTGGGCGGTGGGGGGAGACCGACTCACTTGAGTTT
                                                                                              GTCACAGCCCCTCAACCACTGAGGTGTGGGGGGGGTAGGGATCTGCATTTCTTCATATCAA
                                                                                                                                                                                          TTTGGTCACTAACCTTTGCAAGGATACCTTTTTATTTTCTTTAAGATTCCTGTTGTTTAT
                                                                        GTCACAGCCCCTCAACCACTGAGGTGTGGGGGGGTAGGGATCTGCATTTCTTCATATCAA
                                                                                                                                                                     ACACAGATTTTAAGTTTACTCCTACTGCTGACCCAAGTGAAATTCCTTCTCCAGTCACAG
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plate: 12 row: C column: 04
High quality sequence stop: 486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 Eoeun-dong Yuseong-gu, Tel: +82-42-860-4470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +82-42-860-4409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21C Frontier Korean Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Industrial Property (A) the poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toploff by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Toplof, with electroporation method."
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/cell_line="SNU-484"
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/db_xref="taxon:9606"
/clone="S5SNU484s1-12-C04"
/clone_lib="S5SNU484s1"
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Pred. No.
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Best Local Similarity
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                                                                                                       535 CGGTGGGGGAGACCGACTCACTTGAGGTTTCCTGAAGGCTTCCTGGCCTCCAGCCACGTAA 594
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    454
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                                                                                 CGGTGGGGGAGACCGACTCACTTGAGTTTCTTGAAGGCTTCCTGGCCTCCAGCCACGTAA 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLCM2444 row: b column: 18
High quality sequence stop: 487.
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_IIMAGE:6269873"
/clone_Iib="NIH_MGC_100"
/tissue_type="hepatocallular carcinoma, cell line"
/tissue_type="hepatocallular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
/corr; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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100.0%; Pr
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                                                                                                                                                                                    Score 414; DB 14; Pred. No. 1.5e-200;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT_6626059 NIH_MGC_116 Homo sapiens 5', mRNA sequence.

BM923267
                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12803 row: e column: 22
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Tissue Procurement: Life Technologies,
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   246
             /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORTG; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally clomed (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NH_MGC Library.*
                                                                                                                                                                                                                                                                                 /clone="IMAGE:5758845"
/clone_lib="NIH_MGC_116"
                                                                                                                                                                                                                                                                    /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match Best Local Similarity

24.78; 99.78;

Score 342; DB 14; Pred. No. 1.2e-163; Mismatches

Length 984;

Indels

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Gaps

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Conservative

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REFERENCE
AUTHORS
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BG749180
BG749180.1 GI
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Plate: LLCM1682 row: n column: 09
High quality sequence stop: 822.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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        245
/Clone_*IMAGE:4844744"
/clone_tib="NIH_MGC_43"
/clone_tib="NIH_MGC_43"
/tissue_type="normal pigmented retinal epithelium"
/tab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; Cloned into ECORI/XhoI sites using the following 5'
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
45 a 322 c 300 g 178 t
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                              GTTTTTCACC
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REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS COMMENT ACCESSION DEFINITION BQ644671/c LOCUS TITLE cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2497 row: j column: 18 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford) 1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian BQ644671.1 EST. AGENCOURT_8490723 NIH_MGC_100 5', mRNA sequence. Contact: Robert Strausberg, Ph.D. Unpublished (1999) Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens BQ644671 BQ644671 GI:21768843 Chordata; Primates; ďď Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. Homo sapiens mRNA Gene linear EST 15-JUL-2002 cDNA clone IMAGE:6293873 Collection (MGC)

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5', mRA sequence.
B0644474
B0644474.1 GI:21768646
               cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2482 row: p column: 21
                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/clone_lib="NIH_MGC_100"
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/lab_host="hH10B (phage_resistant)"
/lab_host="hH10B (phage_resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
EcorI; cDNA made by oligo-dT priming. Directionally cloned
into EcorI/XhoI sites using the following 5; adaptor:
GCACGAG(G). Size-selected >500bp for average insert size
1.8kb Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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/db_xref="taxon:9606"
/clone="IMAGE:6293873"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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AGENCOURT_6729788 NIH_MGC_100
5', mRNA sequence.
BM9278?5
Plate: LLCM2024 row: g column: High quality sequence stop: 750.
Location/Qualifiers
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Tissue Procurement: CGAP (Stanford)
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/note="Organ: liver; Vector: poTB7; Site_1: Abaptor:
/note="Organ: liver; Vector: poTB7; Site_1: Abaptor: liver; Vector: liver;
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                       cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image/image.html
                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                        EST
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                                                                                                                                                                                        Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
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              Insert Length: 1358
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primer:
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/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT prining Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5797671"
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Pred. No. 5.5e-136;
                Std Error: 0.00
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sapiens cDNA clone IMAGE:1456938
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                                                           The sequence contained an oligo-dT track that was present in oligonucleotide that was used to arime the synthesis of first strand cDNA and therefore this may represent a bonafide poly tail. cDNA Library Preparation: M.B. Soares Lab Clone distribucion: CGAP clone distribution information can be found through
                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
1 (bases 1 to 357)
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AW293816.1
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UI-H-BI2-ahp-g-09-0-UI.sl NCI_CGAP_Sub4
IMAGE:2727737 3', mRNA sequence.
                   www-bio.llnl.gov/bbrp/image/image.html
                                         I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Seq primer: M13 Forward
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/note="0rvn"
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/clone_lib="NCI_CGAP_K
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Pred. No. 6.3e-112;
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                                                                                                                                                                 TCATGGATGACGACGC 357
  BF364659 364 bp MR2-NN11111-070800-007-h12 NN11111 BF364659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polylinker; Site_1: Not 1; Site_2: Eco R; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub4 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_Pr28, NCI_CGAP_CO4, NCI_CGAP_Pr22, NCI_CGAP_Kid3, NCI_CGAP_Kid41, NCI_CGAP_Kid41, NCI_CGAP_Kid41, NCI_CGAP_Kid41, NCI_CGAP_LO4, NCI_CGAP_EX, NCI_CGAP_CO4, NCI_CGAP_EX, NCI_CGAP_CO5, NCI_CGAP_CO5, NCI_CGAP_LO4, NCI_CGAP_LO
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1 92 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="DH10B (Life Technologies)"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.
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Pred. No. 7.2e-89;
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                        Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 357;
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                                                linear
                        mRNA sequence.
                                                EST 24-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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SOURCE
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BG750306/c
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 142;
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                                           BG750306.1
                                                                                         mRNA sequence.
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                                                GI:14060959
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VERSION
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                                                                                                                                                                                                                                                                                                                                                      990 TAACGGCCGTGCGCCTAGGCGTCCACCCAGAGGAGACACTAGGAGCTTGCAGGACTCGGA 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                930 GGCGCGGGATCGCCTCCTGAAACGAACGAGAACTGACGAATCCACAGGTGAAAGAGAAG 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 GGCGCGGGATCGCCTCCTGAAACGAACGAGAAACTGACGAATCCACAGGTGAAAGAGAAG 146
                                                                                                                                                                                           TAACGGCCGTGCGCCTAGGCCGTCCCAGCCCAGAGGAGACACTAGGAGCTTGCAGGACTCGGA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 364)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Ragai,M.A., da Silva,W. Jr., Zago,M.A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2-MR2-NN11111-
070800-007-h12&t3=2000-08-07&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
BG750306 835 bp mRNA linear EST 15-MAY-2001 602709116F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4845915 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF364659.1 GI:11326684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-*Organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NN1111"
/dev_stage="Adult"
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100.0%; Pr
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Pred. No.
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REFERENCE
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Search completed: January 18, 2003, 23:34:29 Job time : 2221 secs
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                                                                                                                                                                                                                                                                                                              Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                             Query Match 10.3%;
Best Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                               753 GCGCCCCGCGTAGAAGGGGTCCCCGTTGCGGTACACAAGCACGCTCTTCACGACGGGCTG 812
                                                                                                                                                                                   AGACAGGTGGCTGGACCTGGCGCTGCCGCTCATCTTCCCCGCTGGCCGCCGCCCTCAG 872
                                                                                                                                                                                                                                                 CTCGCTGCTTCGCGTCGGGAGGCACCTCCGCTGTCCCAGCGGCCTCACCGCACCCAGGGC 634
                                                                                                                                           CTCGCTGCTTCGCGTCGGGAGGCACCTCCGCTGTCCCAGCGGCCCTCACCGCACCCAGGGC 932
                                                               GCGGGATCGCCTC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L/LCM1685 row: o column: 04
High quality sequence start: 118
High quality sequence stop: 812.
1. 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 835)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                          216 a
                                                                                                                                                                                                                                                                                                                                                                                  Score 142; DB 12; Length 835; Pred. No. 3.5e-61; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                              Gaps
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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 18, 2003, 21:56:44; Search time 119 Seconds

(without alignments)

Sin 8.067 Million cell updates/sec

Title: US-09-674-593-1

Perfect score: 1382
Sequence: 1 cattatgctaecagcataea......taeagcaettaegttcctgg 1382
Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 393868 seqs, 222934149 residues

Word size: 0

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 2000000000
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Published_Applications_NA:*

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14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

Post-processing: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 261, App	Sequence 3, Appli	Sequence 742, App	Sequence 222, App	Sequence 394, App	Sequence 3, Appli	Sequence 3, Appli		Sequence 447, App			Sequence 448, App	Sequence 447, App	Sequence 448, App	Sequence 12891, A	Sequence 726, App	Sequence 55, Appl	Sequence 3, Appli	Sequence 6, Appli
OI .	US-09-925-297-261	US-09-813-320-3	US-09-954-531-742	US-09-954-456-222	US-09-954-456-394	2 US-10-060-333-3	US-09-729-920-3	US-09-969-373-1071	US-09-946-807-447	US-09-946-807-448	US-09-795-668-447	US-09-795-668-448	US-09-795-686-447	US-09-795-686-448) US-09-960-352-12891	US-09-954-531-726	US-09-817-607-55	US-09-977-221-3	US-09-927-091-6
DB	10	10	6	10	10	12	10	10	0	6	10	10	10	10	10	σ	10	6	10
Length	2116	397658	447	511	511	38844	143306	359	401	401	401	401	401	401	433	501	933	11270	45845
Query Match	2.0		1.8	1.8	1.8	1.8	1.8	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
Score	28	27	25	25	25	25	25	24	24	24	24	24	24	24	24	24	24	24	24
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	Query Score Match Length DB ID	Score Match Length DB ID 28 2.0 2116 10 US-09-925-297-261	Score Match Length DB ID 28 2.0 2.116 10 US-09-925-297-261 27 2.0 397658 10 US-09-813-320-3	Score Match Length DB ID 28 2.0 2116 10 US-09-925-297-261 27 2.0 397658 10 US-09-913-320-3 25 1.8 447 9 US-09-954-531-742 SS	Acore Match Length DB ID 28 2.0 2116 10 US-09-925-297-261 27 2.0 397658 10 US-09-954-320-3 25 1.8 447 9 US-09-954-456-222 35 1.8 511 10 US-09-954-456-222	Acore Match Length DB ID 28 2.0 2116 10 US-09-925-297-261 27 2.0 397658 10 US-09-913-320-3 25 1.8 447 9 US-09-954-456-222 25 1.8 511 10 US-09-954-456-222	Score Match Length DB ID 28 2.0 2116 10 US-09-25-297-261 27 2.0 397658 10 US-09-954-297-261 25 1.8 447 9 US-09-954-531-742 25 1.8 511 10 US-09-954-456-222 25 1.8 511 10 US-09-954-456-394 25 1.8 38844 12 US-10-060-333-3	Score Match Length DB ID 28 2.0 2116 10 US-09-925-297-261 27 2.0 397658 10 US-09-931-320-3 25 1.8 447 9 US-09-954-456-222 25 1.8 511 10 US-09-954-456-394 25 1.8 38844 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401 10 US-09-966-873-1071 24 1.7 401 10 US-09-966-874 24 1.7 401 10 US-09-956-68-447 24 1.7 401 10 US-09-755-686-447 24 1.7 401 10 US-09-755-686-448 24 1.7 401 10 US-09-755-686-448 25 1.8 31 10 US-09-755-886-448 26 1.7 401 10 US-09-755-886-448 27 1.7 401 10 US-09-755-886-448 28 1.7 401 10 US-09-755-886-448 29 1.7 401 10 US-09-755-886-448 21 1.7 401 10 US-09-755-886-448 22 1.7 401 10 US-09-755-886-448 23 1.7 401 10 US-09-755-886-448 24 1.7 401 10 US-09-755-886-448 25 1.7 401 10 US-09-755-886-448 26 1.7 401 10 US-09-755-886-448 27 1.7 401 10 US-09-755-886-448 28 1.7 401 10 US-09-956-055-21-2891 29 1.7 501 9 US-09-977-221-3

Sequence 4, Appli Sequence 17, Appl Sequence 10, Appl Sequence 3, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 20, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 1268, Ap Sequence 1268, Ap Sequence 94, Appl Sequence 284, App	sequence 284, App Sequence 751, App Sequence 751, App Sequence 751, App Sequence 751, App Sequence 369, App	Sequence 2028, Ap Sequence 2029, Ap Sequence 6063, Ap Sequence 197, App Sequence 382, App Sequence 382, App
10 US-09-927-091-4 10 US-09-782-378A-17 12 US-10-003-806-10 9 US-10-026-188-3 10 US-09-949-654-3	10 US-09-949-654-3 9 US-09-771-208-20 1 9 US-09-946-807-1 1 10 US-09-795-668-1 1 10 US-09-795-686-1	10 US-09-920-300A-1268 12 US-10-033-528-1268 9 US-09-920-455-94 9 US-10-025-380-284	9 US-10-023-380-731 10 US-09-922-217-284 10 US-09-922-217-751 10 US-09-833-263-284 10 US-09-833-263-751 9 US-10-040-739-369	10 US-09-764-869-2028 10 US-09-764-869-2029 10 US-09-960-352-6063 9 US-10-040-739-197 10 US-09-917-800A-382 10 US-09-954-456-1350
49744 56737 173808 249487 368004	368004 659158 1503841 1503841	73 73 231 288	7 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	399 399 422 476 476
7.1. 7.1. 7.1. 7.1.	7.1 7.1 7.1 7.1	7.1 7.1 7.1 7.1		7.11 7.11 7.11 7.11
22222 24444	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	7 7 7 7 7 7	3 3 3 3 3 3 3 5 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	333333 5555 7555 7555 7555 7555 7555 75
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ALIGNMENTS

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RESULT 1

US-09-925-297-261

US-09-925-297-261

US-09-925-297-261

Sequence 261, Application US/09925297

FREERIN US-050081659A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

FRIOR APPLICATION NUMBER: PCT/US00/05989

FRIOR APPLICATION NUMBER: PCT/US00/05989

FRIOR APPLICATION NUMBER: PCT/US00/05989

FRIOR APPLICATION NUMBER: PCT/US00/05989

FRIOR FILING DATE: 1999-03-12

NUMBER OF SEO ID NOS: 928

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: PATENTIAL TON: Requals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (4)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (15)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

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OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

NAME/KEY: misc feature

LOCATION: (35)

OTHER INFORMATION: nequals a,t,g, or c

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US-09-925-297-261

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US-09-925-297-261

ONE OTHER INFORMATION: nequals a,t,g, or c

US-09-925-297-261
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PACIENT NO. 0220020113037A1

APPLICANT: Young, Paul
TITLE OF INVENTION:
PROCESS for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C TITLE OF INVENTION: Sets
FILE REFERENCE: 68920-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001.09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR PILING DATE: 2000-09-26
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
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8-09-954-456-394/c
; Sequence 394, Application US/09954456
; Patent No. US20020115057A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 CACACACACACACACACAAATAT 378
                                                                                                                                                  ; Sequence 222, Application US/09954456
; Patent No. US20020115057A1
   395 CACACACACACACACACAAATAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.0
SEQ ID NO 222
LENGTH: 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                         RESULT 4
US-09-954-456-222/c
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Sequence 742, Application US/09954531

Sequence 742, Application US/09954531

Sequence 742, Application US/09954531

Sequence 742, Application US/09954531

Sequence 742, Application Application US/099954

TITLE OF INVENTION: Cone Sets

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION UNMBER: US/00/25-02

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR APPLICATION NUMBER: US/60/234,567

PRIOR PRILING DATE: 2000-09-22

PRIOR PRILING DATE: 2000-09-22

PRIOR PRILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 1392

SOCTWARRE: PatentIn version 3.0
                                                                                                                                                                     %Sequence 3, Application US/09813320

Sequence 3, Application US/09813320

Sequence 3, Application US/09813320

Patent No. US20020142378A1

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/813,320

CURRENT APPLICATION NUMBER: US/09/813,320

CURRENT FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASELSEQ for Windows Version 4.0
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100.0%; Pred. No. 0.0091;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0013;
tive 0; Mismatches 0;
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1.8%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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1225 CGCACACACACACACACACAAATATG 1252
                               204 CGCACACACACACACACACAAATATG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1224 ACGCACACACACACACACACAAATA 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1227 CACACACACACACACACAAATAT 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (1)...(397658); OTHER INFORMATION: n = A,T,C or G US-09-813-320-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 27; Conservative
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ORGANISM: Homo sapiens
US-09-954-531-742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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LENGTH: 397658
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                                                                                                                                                                                                         1.8%; Score 25; DB 10; Length 143306; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: SOPDean SSRs and Methods of Genotyping
FILE REPERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-13
PRIOR FILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1071
LENGTH: 359
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Patent No. US200201651441

GENERAL INFORMATION:

APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.

TITLE OF INVENTION: HUMBAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001

CURRENT APPLICATION NUMBER: US/09/946,807

CURRENT FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2000-02-28

PRIOR PLILING DATE: 2000-02-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 447
LENCTH: 401
       NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 143306
                                                                                                                                                                                                                                                                                                                                       Db 18457 CACACACACACACACACAAATAT 18433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1071, Application US/09969373
Patent No. US20020133852A1
; GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
                                                                                                                                                                                                                                                                                                             1227 CACACACACACACACACAAATAT 1251
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                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 25; Conservative
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US-09-946-807-447
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                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-969-373-1071/c
                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-729-920-3
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APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILLE OF INVENTION: USES THEREOF
FILLE REFERENCE: CLO00862DIV
CURRENT APPLICATION NUMBER: US/10/060,333
CURRENT FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASISEO for Windows Version 4.0
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APPLICANT: GUEGLER, MATI et al
APPLICANT: GUEGLER, MATI et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/729,920
CURRENT FILING DATE: 2000-12-06
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PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTHARE: PALENTIN VERSION 3.0
SEQ ID NO 394
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Patent No. US20020115186A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KRS: misc_feature
CTHER INFORMATION: n=a,t,g or c
US-09-954-456-394
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-060-333-3
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Sequence 448, Application US/09795668 Patent No. US20020045577A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-795-686-447
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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US-09-795-686-448
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US-09-795-686-447
                                        US-09-795-668-448
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US-09-795-668-448
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LENGTH: 401
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                     Length 401;
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                                                           Indels
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Score 24; DB 9; Len; Pred. No. 0.029;
                                                                                                                                                                                                                                       Sequence 448, Application US/09946807
Patent No. US20020165144A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefinthorsdottir, Valgerdur
APPLICANT: Guicher, Jeffrey R.
TITLE OF INFORTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-8
NUMBER OF SEQ ID NOS: 1531
SOFTWARE FEASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanthorsdottir, Valgerdur
APPLICANT: Glother, Jaffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 447
              Query Match 1.7%; Score 24; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 24; Conservative 0; Mismatches
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                                                                                                 1227 CACACACACACACACACAAATA 1250
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CORGANISM: Homo sapiens
US-09-946-807-448
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Matches 24; Conserv
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US-09-946-807-448
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LENGTH: 401
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Patent No. US20020094954a1

GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR PILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FASLSEQ for Windows Version 4.0
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanthorsdottir, Valgerdur
APPLICANT: Glincher, Jaffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 448
LENGTH: 401
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Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Olicher, Joffrey R.
TILE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
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RESULT 15
US-09-960-352-12891
US-09-960-352
US-09-960-352-12891
Sequence 12891, Application US/09960352
Fatent No. US-2002013713941
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12891
LENGTH: 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA GRANISM: BOS taurus OTHER INFORMATION: Clone ID: 55-LIB3058-019-Q1-K1-F12 US-09-960-352-12891
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,715
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 448
LENGTH: 401
TYPE: DNA
CNEGANISM: HOMO Sapiens
US-09-795-686-448
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Job time: 521 secs
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AAZ36643 standard; cDNA; 1382 BP.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	AAA7426 AA19064 ABL6347 ABQ5777 AA18629 ABL6491		ABL134295 AAS46349 AAS46349 ABL3213 AAS61168 ABK31258 ABK31258 ABK31258 AAA88864	ABQ7353 ABL7038 AAS6133 ABK3142 ALIGN
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complement (1280..1305)
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/note= "binding site for primer VDE120 (see AA236648)"
                                                                                   Antisense; human; tumour rejection antigen; RUR-1; tumour; cancer; renal cell carcinoma; colorectal carcinoma; melanoma; sarcoma; leukaemia; ss.
                                           Human tumour rejection antigen RUR-1 antisense cDNA sequence.
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22-FEB-2000 (first entry)
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Location/Qualifiers
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                                                                                                                                   The present sequence represents the antisense cDNA sequence of human tumnour rejection antigen RUR-1. The present sequence is the antisense strand of a ubiquitously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumnour samples and tumnour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal call carcinoma, colorectal carcinoma, melanoma, sarcoma or leukaemia.
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                                                                                       tumour rejection antigen RUR-1 nucleic acids, used
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                                       Boon-Falleur
                  (LUDW-) LUDWIG INST CANCER RES
                                                                                                                   Claim 4; Fig 5; 75pp; English.
98US-0085318
                                                                                                e.g. treatment of cancers
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P-PSDB; AAY53809.
                                      Eynde B,
                                                                                       New isolated
13-MAY-1998;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                              976 AGGIGAAAGAGAAGIAACGGCCGIGCGCCIAGGCGICCACCCAGAGGAGACACIAGGAGC 1035
                                                                                       036 TTGCAGGACTCGGAGTAGACGCTCAAGTTTTTCACCGTGGCGTGCACAGCCAATCAGGAC 1095
                                                                                                                                                                                                                                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzhehmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                            CCGCAGTGCGCGCACCACACCAGGTTCACCTGCTACGGGCAGAATCAAGGTGGAC 1150
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Zhang J;
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Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                              AAI58192 standard; cDNA; 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
2000US-0693036.
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                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAM39036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200153312-A1.
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14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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Zhao QA,
                                                                                                                                                                                                                                                                                            AAI58192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ubiquitously expressed gene. The antisense strand of the present sequence encodes tumour rejection antigen RUR-1. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The antisense sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or
                       484.501
/*tag= b
/note= "binding site for primer VDE87 (see AA236645)"
                                                                                       /*tag= c
/note= "binding site for primer VDE93 (see AAZ36646)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                       New isolated tumour rejection antigen RUR-1 nucleic acids, used for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents the sense cDNA sequence of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an expression product, such as cancers, e.g. renal cell carcinoma, colorectal carcinoma, melanoma, sarcoma or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTAGCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGTAGATGTTCCTGACGCCCCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGCCTGAACGCCGCCGGTCACCTCCTTCAGGAAGACTTCGAAGCTGGACACCTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATGGATGACGACGCGCGCCCCGCGTAGAAGGGGTCCCCGTTGCGGTACACAAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGCCGCCGCCTCAGCTCGCTGCGTCGGGAGGCACCTCCGCTGTCCCAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTTCACGACGGGCTGAGACAGGTGGCTGGACCTGGCGCTGCTGCCGCTCATCTTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGCCGCCGCCTCAGCTCGCTTCGCGTCGGGAGGCACCTCCGCTGTCCCAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.1%; Score 595; DB 21; Length 2167; 100.0%; Pred. No. 1.5e-282; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2167 BP; 675 A; 440 C; 576 G; 476 T; 0 other;
                                                                          complement (917..935)
                                                                                                                                                                                                                                                                                          Van Den Eynde B, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Fig 6; 75pp; English.
                                                                                                                                                                                                                                98US-0085318.
                                                                                                                                                                                                 99WO-US10424
                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER
                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancers
303..1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 595; Conservative
              /*tag=
                                                                                                                                                                                                                                                                                                                       WPI; 2000-053076/04.
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                                                                                                                                     WO9958546-A1
                                                                                                                                                                                                 13-MAY-1999;
                                                                                                                                                                                                                              13-MAY-1998;
                                                                                                                                                                   18-NOV-1999.
                              primer_bind
                                                                         primer_bind
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Wang D;

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Homo sapiens.
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                                                                                     Claim
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AAI59978/c
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         and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
                                Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                         915
                                                                                                               615
                                                                                                                                               675
                                                                                                                                                        CTCTTCACGACGGGCTGAGACAGGTGGCTGGACCTGGCGCTGCTGCTGCTGCTCTTCCCC 855
                                                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                       234
                                                                                                                                                                                                                                                                                                                         676 GGTGCCTGAACGCCGCCGGTCACCTCCTTCAGGAAGACTTCGAAGCTGGACACCTTCTTC 735
                                                                                                                                                                                                                  TCATGGATGACGACGCGCCCCCCGTAGAAGGGGTCCCCGTTGCGGTACACAAGCACG 795
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; human; tumour rejection antigen; RUR-1; tumour; cancer; renal cell carcinoma; colorectal carcinoma; melanoma; sarcoma; leukaemia; EST; expressed sequence tag; ss.
                                                                                                                                              TCTAGCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGTAGATGTTCCTGACGGCCCCAAAG
                                                                                                                                                                                                                                                             GCTGGCCGCCGCCTCAGCTCGCTGCTTCGCGTCGGGAGGCACCTCCGCTGTCCCAGCGGC
                                                                                                             TTGAGTTTCTTGAAGGCTTCCTGGCCTCCAGCCACGTAATTGCCCCCGCTCTGGATCTGG
                                                                                                                                                                                                                                                                                               293 GCTGGCCGCCTCAGCTCGCTGCTTCGCGTCGGAGGACCTCCGCTGTCCCAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST AA863443 which overlaps the RUR-1 antisense cDNA sequence.
                                                                            Length 1956;
                                                                                              0; Indels
                                                          Sequence 1956 BP; 540 A; 435 C; 541 G; 435 T; 5 other;
                                                                           36.0%; Score 498; DB 22; L
100.0%; Pred. No. 8.8e-235;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                            TTGCAGGACTCGGAGTAG 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     TIGCAGGACTCGGAGTAG
                                                                                    Similarity
                         C.N.S disorders.
                                          specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                           Query Match
Best Local Simi
Matches 498;
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The present sequence represents an expressed sequence tag (EST) which overlaps the antisense CDNA sequence of human tumour rejection antigen RUR-1. The RUR-1 antisense sequence is the antisense strand of a ubiquitcously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour derived cells lines. The polypeptide is unrelated to any TRAP protein. The RUR-1 sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal cell carcinoma, colorectal carcinoma, melanoma, sarcoma or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note: although the present sequence is mentioned in claim 8, it is not specifically claimed. The fragments of AAZ36643-44 which DO NOT contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                                                                                                                           New isolated tumour rejection antigen RUR-1 nucleic acids, used for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 CCTCAACCACTGAGGTGTGGGGGGGTAGGGATCTGCATTTCTTCATATCAACCCCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 TTAAGTTTACTCCTACTGCTGACCCAAGTGAAATTCCTTCTCCAGTCACAGTGTAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 246 BP; 63 A; 66 C; 44 G; 73 T; 0 other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present sequence are claimed.
                                                                                                                                                                                                                                                                                                                                  8; Page 71; 75pp; English.
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(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                             e.g. treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                              WPI; 2000-053076/04
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09-MAR-2001 (first entry)
                                                                                           WO200210449-A2
                                                                       Homo sapiens.
                                                                                                                    07-FEB-2002.
                                                                                                                                                                                                                             Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC99033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, lumunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system inseases, such as localised neuropathies and central nervous system diseases, such as lateral society, and Shybrager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and crows of the activity, arthritis and inflammation, leukaemias and crows of the activity, arthritis and inflammation, leukaemias and crows of the activity, arthritis and inflammation, leukaemias and crows of the activity, arthritis and inflammation, leukaemias and crows of the activity arthritis and inflammation, leukaemias and crows of the activity arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                   Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        556 TTGAGTTTCTTGAAGGCTTCCTGGCCTCCAGCCACGTAATTGCCCCCGCTCTGGATCTGG 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTAGCTTCCGGATTCGGTGGCCAGTCCGCGGGGTGTAGATGTTCCTGACGGCCCCAAAG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, W
Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.1%; Score 139; DB 22; Length 492; 100.0%; Pred. No. 5e-58; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                 Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 492 BP; 145 A; 111 C; 132 G; 100 T; 4 other;
                                                                                                                                                                                                              Liu C, Asundi V, Chen R, Ma Y, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 3967; 10078pp; English.
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                                                                                                                             2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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                                                        26-DEC-2000; 2000WO-US34263
                                                                                                         2000US-0598042
                                                                                                                   20000S-0620312
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Matches 139; Conservative
                                                                                                                                                                                                                                                             WPI; 2001-442253/47.
                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                             P-PSDB; AAM40822
          WO200153312-A1
                                                                                                                                         14-SEP-2000; 29-OCT-2000; 29-NOV-2000;
                                                                                           25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                              03-AUG-2000;
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                                26-JUL-2001
                                                                                                                                                                                                                                          Zhao QA,
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                                                                                                                                                                                                                             Wang
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ABN38745
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises cerveral oligonucleotides, each capable of hybridising selectively to a several oligonucleotides, each capable of hybridising selectively to a cerver of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a blological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal conscriptions. The libraries may also be used as specialised minical conscription of detect transcripts of a sub-transcriptome and in particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA cranscripts and splice variants of a transcriptome of a pattient suffering from a particular disorder. ABN27253 to ABN59589 represent coligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present liventic format directly from WIPO condition in the was obtained in electronic format directly from WIPO condition in the was obtained in electronic format directly from WIPO condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         938 ATCGCCTCCTGAAACGAACGAGAAACTGACGAATCCACAGGTGAAAGAGAGAAGTAACGGCC 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                        RNA transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligonucleotide libraries comprising oligonucleotides which
                                                                                   Human; mouse; rat; splice transcript; detection; RNA transo splice variant; transcriptome; oligonucleotide library; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 60; DB 24; Pred. No. 3.9e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wasserman A, Mintz E, Mintz L,
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Matches 60; Conservative
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food additive;

cancer related protein; HISBL55;

(first entry)

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Human cDNA clone HISBL55 encoding cancer related protein 21.
              04-JUL-2001
 AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AB54666. The human pancreatic cancer antigens have cytostatic, cauched human pancreatic cancer antigens have cytostatic, cauched the human pancreatic cancer antigens have cytostatic, cantraceptive, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used for in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to design nucleic detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be screened for. The pancreatic cancer antigen polynucleotides can be used to design nucleic and diagnostic methods. The proteins can be used to design nucleic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal or prevent ceproductive disorders. AAC99234 ond AAB54467 represent sequences used in the exemplification of the present invention.
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                                                        detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antlinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
              Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:261
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                                             pancreas; pancreatic cancer; pancreatic cancer antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 699-700; 1379pp; English.
                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 08;
                                                                                                                                                                                                                                                         08-MAR-2000; 2000WO-US05989.
                                                                                                                                                                                                                                                                                       99US-0124270.
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                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-579444/54.
                                                                                                                                                                                                                                                                                                                                                  Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                             40200055320-A1
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                       12-MAR-1999;
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The sequence encodes a novel Human cancer related protein. The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, treating or ameliorating a medical condition in e.g. humans.

The color of the color of cancer (e.g. daditive or preservative to polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotide are useful for chromosome identification. The nucleic acids, protein, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of cancer (e.g. cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital), immune disorders (e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, acquired immunodeficiency syndrome, AIDS), cardiovascular disorders such as myocardial ischaemias, wound healing, neurological disorders such as myocardial ischaemias, wound healing, neurological and epilepsy) and infectious diseases uch as viral, bacterial, fungal and parasitic infections. Numerous examples of each type of disorder are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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preservative; immunogen; antibody; bone cancer; adrenal cancer; bone marrow cancer; breast cancer; gastrointestinal cancer; liver cancer; luce and cancer; luce cancer; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple solenosis; heumaroid arthritis; ulcerative collitis; myocardial ischaemia; wound healing; neurological disorder; parkinson's disease; Alzehmer's disease; cerebral anoxia; epilepsy; viral infection; bacterial infection; fungal infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Cancer related protein 21"
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100.0%; Pred. No. 0.0022;
Live 0; Mismatches 0;
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99US-0158003.
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Matches 28; Conservative
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AAS00847 standard; cDNA; 2116 BP

RESULT 8 AAS00847

AAS00847;

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20000S-0231414
20000S-0232080
20000S-0232080
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2000US-0241816
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2000US-0237037.
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2000US-0246613.
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2000US-0249244
08-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
14-SEP-2000;
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29. SEP-2000;
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29. SEP-2000;
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29. SEP-2000;
29. SEP-2000;
20. CCT-2000;
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17-NOV-2000;
17-NOV-2000;
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21-SEP-2000;
21-SEP-2000;
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    Human; cytostatic; antidiabetic; antiinflammatory; gastric; osteopathic; antihormone; antiulcer; thyroid-active; gene therapy; antisense therapy; pancreatic cancer; pancreatitic; pancreatitis; diabetes; endocrine disorder; acromegaly; hyperthyroidism; gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.
                                                                                                                                                                                       Human pancreatic cancer related genomic DNA, SEQ ID NO: 446
 1225 CGCACACACACACACACACAAATATG 1252
                ABA07127 standard; DNA; 2219
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2000US-0205515
2000US-0219467
2000US-0215135
2000US-0215135
2000US-0217487
2000US-0217487
2000US-0217496
2000US-0217496
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2000US-0226279.
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2000US-0225268.
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2000US-0230437.
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2000US-0228924
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                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                 WO200155206-A1
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04 - FEB - 2000;

02 - MAR - 2000;

16 - MAR - 2000;

17 - MAR - 2000;

18 - APR - 2000;

19 - MAY - 2000;

19 - MAY - 2000;

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06-SEP-2000;
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ABA07127
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17-JAN-2001; 2001WO-US01324
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16-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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30-AUG-2000;
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29-SEP-2000;
                  02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polypeptide comprising an amino acid sequence at least 90% identical to 188 amino acid sequences fully defined in the specification and encoded by 188 cDNA clones fully defined in the specification. The invention also relates to a fragment having biological activity, a domain, an epitope, full length protein, variant, allelic variant or a species homologue of the fully defined sequence. The polynucleotide and polypeptide are useful for treating, preventing and/or prognosing disorders related to the pancreas including pencreatic cancer, pancreatitis, diabetes, endocrine disorders such as acromegaly or hyperthyroidism, and gastrointestinal disorders such as crohn's disease and duodenal ulcers. The present sequence encodes a pancreatic cancer-related polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated pancreatic cancer polypeptide for treating, preventing and/prognosing disorders related to the pancreas including pancreatic cancers and also for testing and detection e.g. diagnosis -
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100.0%; Pred. No. 0.0022;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 446; 537pp; English.
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                          17-NOV-2000; 20000S-024926; 17-NOV-2000; 20000S-024926; 17-NOV-2000; 20000S-024926; 17-NOV-2000; 20000S-024929; 17-NOV-2000; 20000S-02499; 17-NOV-2000; 20000S-02499; 17-NOV-2000; 20000S-025099; 17-NOV-2000; 20000S-0251988; 17-NOS-2000; 20000S-0251869; 18-DEC-2000; 20000S-0251869; 18-DEC-2000; 20000S-0251869; 18-DEC-2000; 20000S-0251869; 18-DEC-2000; 20000S-0251869; 11-DEC-2000; 20000S-0251869; 11-DEC-2000; 20000S-0251899; 11-DEC-2000; 20000S-0251999; 11-DEC-2000; 20000S-0251999; 11-DEC-2000; 20000S-0251999; 11-DEC-2000; 20000S-0251990; 11-DEC-2000; 20000S-025190; 11-DEC-2000;
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The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Mackel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.

Sequence 2219 BP; 618 A; 507 C; 409 G; 685 T; 0 other;

Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -

WPI; 2001-502630/55

Disclosure; SEQ ID NO 2917; 986pp; English

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2000US-0241808.
2000US-0241809.
2000US-0241826.
2000US-0244617.
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2000US-0246475.
2000US-0246476.
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2000US-0249212.
2000US-0249213.
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2000US-0249215.
2000US-0249216.
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2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249300.
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2000US-0237038.
2000US-0237039.
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2000US-0239335.
2000US-0239937.
2000US-0240960.
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2000US-0246613.
2000US-0249207.
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2000US-0246528.
2000US-0246532.
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2000US-0251990.
2000US-0254097.
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2000US-0246610.
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2000US-0249245.
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2000US-0241785
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2000US-0246526.
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2000US-0251479
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                                           29 - SEP - 2000;
02 - CCT - 2000;
02 - CCT - 2000;
03 - CCT - 2000;
13 - CCT - 2000;
13 - CCT - 2000;
20 - C
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08-DEC-2000;
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08-DEC-2000;
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05-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; account ocerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                 Human cDNA differentially expressed in granulocytic cells #31.
                                                                                                                                                                                                                                                                                                                                               viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
Score 28; DB 22; Length 2219;
Pred. No. 0.0022;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                   Human; ss; granulocytic cell; DNA chip; bacterial infection;
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                   100.0%; Pred. No. 0.0
live 0; Mismatches
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                                                                       1225 CGCACACACACACACACACAAATATG 1252
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                                                                                        462 CGCACACACACACACACAAATATG 489
                                                                                                                                                                                            ABK83460 standard; cDNA; 165199 BP
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   2.0%;
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                   Best Local Similarity 100.
Matches 28; Conservative
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       Query Match
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ABK83460/c
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Ruben SM;

Barash SC,

Rosen CA,

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2001-514838/56.
                                  P-PSDB; AAO02105
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Also included are modulating (M2) GA by contacting GC with an agent that a alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammation disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA, M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation (especially chronic) in a tissue, an allergic detecting an inflammation (especially chronic) in a tissue, an allergic
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                                                                                                                                                                                                                                                                                                   response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, pariodontal disease, also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemla; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%; Score 28; DB 24; Length 165199;
ilarity 100.0%; Pred. No. 0.0021;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 17664 AGGACGCACACACACACACACACAAA 17637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1221 AGGACGCACACACACACACACACAAA 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 2096.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI82036 standard; cDNA; 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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les 28; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein-encoding gene 28 cDNA clone HNGPM78, SEQ ID NO:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; proliferative disorder; cancer; tumour; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer; a disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotraris; food additive; gene therapy; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                                    Claim 1; SEQ ID NO 2096; 1399pp + Sequence Listing; English.
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0.021;
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/product= "Human secreted protein"
307..366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 CACACACACACACACACAAATATG 203
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367..381
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les 26; Conservative
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17-JAN-2001; 2001WO-US01354
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2000US-0190076
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                              WO200157182-A2
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19-MAY-2000;
20-JUN-2000;
30-JUN-2000;
30-JUL-2000;
07-JUL-2000;
11-JUL-2000;
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23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-JUL-2000;
26-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
   Homo sapiens.
                                                                                                                                                                          16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
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14-AUG-2000;
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                                                         09-AUG-2001
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   9\times28\times6\times26\times6
                                                                                                                                                                                                                                                                     AAD AAD05300-AAD05379 represent cDNAs corresponding to 28 human secreted protein genes, and AAE01436-AAE01513 represent the proteins they encode. AAE01514-AAE01544 represent human secreted protein fragments or variants. CC AAE01514-AAE01544 represent human secreted protein fragments or variants. The genes and their secreted proteins are useful for preventing. The genes and their secreted proteins are useful for preventing. CC treating or ameliorating medical conditions, e.g., by protein or gene that a protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the amount of the new genes. Specific uses are described for each of the proliferative disorders, cancer, tumours, foetal and developmental abnormalities, heamatopoletic disorders, diseases of the immune system, ALDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, diseases, cardiovascular disorders, angiogenic disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, pregnancy-related disorders, and infections. The proteins can also be used to aid wound health organs before transplantation, for supporting cell culture of parimary tissues. To remain the content of prevent skin aging cell culture of parimary tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                     New nucleic acid molecules encoding 28 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunossays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38676.
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                                                                                                                    Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1747 BP; 407 A; 481 C; 476 G; 383 T; 0 other;
                                                                                                                 Ruben SM, Komatsoulis GA, Moore PA, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein-encoding cDNA of the invention.
                                                                                                                                                                                                                                                Claim 1; Page 443-444; 562pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1227 CACACACACACACACACAAATATG 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK83864 standard; DNA; 16584 BP
                                          05-NOV-1999; 99US-0163581.
30-JUN-2000; 2000US-0215133.
                                                                                    (HUMA-) HUMAN GENOME SCI INC
               01-NOV-2000; 2000WO-US30045.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-NOV-2001 (first entry)
                                                                                                                                             WPI; 2001-308778/32
                                                                                                                                                              P-PSDB; AAE01463
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2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249300.
2000US-0250160.
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
20-CGT-2000;
                                                     02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
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20-0CT-2000;
20-0CT-2000;
01-0NO-2000;
08-NOV-2000;
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20-0CT-2000;
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17 - NOV - 2000;
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17-NOV-2000;
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cartivity, and can be used in AAM91201. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) cartivity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) capplement the patients own produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted Lio express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic acids and cancer metastases of haematopoietic actived cells. AAK64703 to AAK87694 represent human immune/haematopoietic actived cells. AAK64703 co AAK87695 and AAM88169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        represent sequences used in the exemplification of the present invention
                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; human; tumour rejection antigen; RUR-1; tumour; cancer; renal cell carcinoma; colorectal carcinoma; melanoma; sarcoma; leukaemia; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR primer VDE119 used to amplify RUR-1 antisense cDNA sequence.
                                                                                                                                                                        Disclosure; SEQ ID NO 38676; 3071pp + Sequence Listing; English.
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Pred. No. 0.021;
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                  Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 1.9%
Best Local Similarity 100.0
Matches 26; Conservative
                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-053076/04.
                                                      WPI; 2001-483426/52
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e.g. treatment of cancers -

(HUMA-) HUMAN GENOME SCI INC

Example 1; Page 44; 75pp; English.

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                                                           PCR primers AA226647-48 were used to amplify the antisense cDNA sequence of human tumour rejection antigen RUR-1. The RUR-1 antisense sequence is the antisense strand of a ubiquitously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder an expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal cell carcinoma, melanoma, sarcoma or leukaemia.
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1.8%; Score 25; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 25; Conservative 0; Mismatches 0; Indels
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Title: Perfect score:

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Run on:

Scoring table:

Searched:

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US-09-488-671-10/C

Sequence 10, Application US/09488671A

Patent No. 6187545

GENERAL INFORMATION:
APPLICANT: Robert M. Butler
APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCR-CYTOSOLIC EXPRESSION
FILE REFERENCE: RTS-0123
CURRENT APPLICATION NUMBER: US/09/488,671A
CURRENT FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 177
SEQ ID NO 100

SEQ ID NO 100
US-09-411-291-3
US-08-998-416-274
US-09-091-49-476-270
US-09-071-035-101
US-08-693174-5
US-08-693174-5
US-09-253-738-5
US-09-25-041-12
US-09-245-041-14
US-09-245-041-14
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LOCATION: (6440)...(6621)
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(7206)...(7409)
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(7682)...(7869)
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LOCATION: (5895)...(6118)
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                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-482-080A-505
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US-09-641-638-633
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US-09-641-638-654
US-08-680-395-4
US-07-674-287B-1
US-08-436-900A-1
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US-08-171-389-505
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US-08-121-446-1
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                                                                                                     January 18, 2003, 23:37:54;
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Maximum Match 100%
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Score 19.8; DE Pred. No. 9; 0; Mismatches

Query Match
Best Local Similarity 91.3%;
Matches 21; Conservative

; NAME/KEY: CDS ; LOCATION: (10701)...(11155) US-09-488-671-10

Sequence Sequence Sequence Sequence

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Sequence Sequence Sequence

US-08-467-126-1 US-08-476-712-3

Length 12141; Indels

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GENERAL INCORMATION:
GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Blumenfeld, Marte
APPLICANT: Chumakov, Ilya
APPLICANTON NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR APPLICATION NUMBER: US 60/133,207
PRIOR PILING DATE: 1999-05-07
PRIOR PILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-03-23
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/119,917
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRING; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
; CURRENT APPLICATION NUMBER: US,09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR FILING DATE: 2000-02-11
; PRIOR FILING DATE: 1999-05-07
; PRIOR FILING DATE: 1999-05-07
; PRIOR FILING DATE: 1999-05-07
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SEQ ID NO 632
; LEGGTH: 1000
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COTHEN INFORMATION: 10-507-321.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 181..199

OTHEN INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 588..607

OTHEN INFORMATION: downstream amplification primer, complement
NAME/KEY: mise_binding
LOCATION: 489..513

OTHEN INFORMATION: 10-507-321 potential probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 10-507-321 : polymorphic base A or C NAME/KEY: misc_binding LOCATION: 481..500 OTHER INFORMATION: 10-507-321.misl, potential
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LOCATION: 501
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Sequence 631, Application US/09641638

GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Cohen, Annick
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENEST: 031CP1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT APPLICATION NUMBER: US/09/6133.200
PRIOR APPLICATION NUMBER: US/09/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-02-12
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SPRIOR FILING DATE: 1999-02-12
SPRIOR FILING DATE: 1999-02-12
SOFTWARE: PALCATION NUMBER: US/0/119,917
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: PALCATION NOS: 1304
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CTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 489..513
COTION: 489..513
USATION: 489..513
USATION: 489..513
USATION: 489..513
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LOCATION: 502..521
OTHER INFORMATION: 10-507-170.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 332..350
OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 739..758
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LOCATION: 501
OTHER INFORMATION: 10-507-170 : polymorphic base A or
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LOCATION: 481..500
OTHER INFORMATION: 10-507-170.mis1, potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AAATGGTGGGGGGGGGGAGAC 227
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APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
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Best Local Similarity 87.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-641-638-632
                                                                                                                                                                                                                                                          RESULT 2
US-09-641-638-631
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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FGREEL NO. 9932099

FGREEL NO. 9932099

APPLICANT: Blumenfeld, Marta
APPLICANT: Bouqueleret, Lydie

APPLICANT: Bouqueleret, Lydie

APPLICANT: Chumakov, Ilya
APPLICANT: Chen, Annick

TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1

CURRENT APPLICANTION NUMBER: US 09/502,330

PRIOR FILING DATE: 1000-08-16

PRIOR FILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-23

PRIOR FILING DATE: 1999-03-21

PRIOR FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 1304

SOFTWARE: Patent.pm

SEQ ID NO 63 4 stent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                           COTHER INFORMATION: 10-507-353: polymorphic base C or T
NAME/KEY: misc_binding
LOCATION: 481.500
COTHER INFORMATION: 10-507-353.misl, potential
NAME/KEY: misc_binding
LOCATION: 502.521
COTHER INFORMATION: 10-507-353.mis2, potential complement
NAME/KEY: primer_bind
LOCATION: 149.167
OTHER INFORMATION: upstream amplification primer
COCATION: 556.575
OTHER INFORMATION: downstream amplification primer, complement
LOCATION: 556.575
OTHER INFORMATION: downstream amplification primer, complement
LOCATION: 489.513
OCHER INFORMATION: 10-507-353 potential probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.8%; Score 19.2; DB 4; Length 1000; Best Local Similarity 87.5%; Pred. No. 14; Matches 21; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_binding
LOCATION: 502.521
OTHER INFORMATION: 10-507-364.mis2, potential complement
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 10-507-364 : polymorphic base C or NAME/KEY: misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 481. 500 OTHER INFORMATION: 10-507-364.misl, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-641-638-634
Sequence 634, Application US/09641638
Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AAATGGGTGGGCGGTGGGGGAGAC 25
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                              LENGIS.

TYPE: DNA
ORGANISM: HOMO Sapiens
FEATURE:
NAME/KEY: allele
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ORGANISM: Homo Sapiens
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LOCATION: 501
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SEQ ID NO 633
LENGTH: 1000
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TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEST. 051CP1
CURRENT APPLICATION UNMER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR PELICATION UNMER: US 09/502,330
PRIOR PELICATION NUMBER: US 09/502,330
PRIOR PELICATION NUMBER: US 09/203.23
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: 1999-05-07
PRIOR FILING DATE: US 09/215,267
PRIOR FILING DATE: US 06/219,917
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OTHER INFORMATION: upstream amplification primer
NAME/KEY: primer_bind
LOCATION: 545.054
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 489.0513
COTHER INFORMATION: 10-507-364 potential probe
US-09-641-638-634
                                                                                                                                                                                                                         DB 4; Length 1000;
                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                      Score 19.2; E
Pred. No. 14;
0; Mismatches
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LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 3124..3297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                10 AAATGGTGGGCGGGGGGGGAAC 33
                                                                                                                                                                                                                                                                                                                  2 AAATGGGTGGGCGGTGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Blumenfeld, Marta
APPLICANT: BougueLeret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
                                                                                                                                                                                                                    Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: exon 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: exon 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: exon
LOCATION: 5552..5633
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LOCATION: 6349..6509
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LOCATION: 7379..7522
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polymorphic base C or	polymorphic base G or	polymorphic base A or G	polymorphic base A or	polymorphic base G or	polymorphic base C or	polymorphic base A or (polymorphic base G or	polymorphic base C or	polymorphic base A or		polymorphic	polymorphic base A or	polymorphic base A or	base C	oase A	polymorphic ba	deletion of CTG	polymorphic base G or	polymorphic base C or	polymorphic base C or 1	polymorphic base C or	polymorphic base A or	polymorphic base A or polymorphic base C or
10-343-278 :	10-343-339 :	10-346-23 :	10-346-141 :	10-346-263 :	10-346-305 :	10-347-74 :	10-347-111 :	10-347-165 :	10-347-203 :				10-348-391 :	10-349-47			10-349-216 :	10-349-224 :	10-349-368 :	10-350-72 :	10-350-332 :		10-507-321 :
Q	ပ	Q	ည	Ö	Ų.	O	; COCATION: 03/3 ; OTHER INFORMATION: ; NAME/KEY: allele : LOCATION: 6429	0	0) OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 6534	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 6611	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 7668	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8608	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8658	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8703	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8777	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8785	; OTHER INFORMATION: ; NAME/KEY: allele ; LOCATION: 8926		0			
																						7 100	
							MAMEARI: MISC_reacute LOCATION: 1755520674 OTHER INFORMATION: 3'regulatory region NAME/KEY: allele	: polymorphic base C or T	: polymorphic base C or T	: polymorphic base C or T	: deletion of C	: variable motif ATTTA or TTTTT	polymorphic base C or T	: insertion of T	polymorphic base G or C	: polymorphic base A or G	: polymorphic base A or G	: polymorphic base C or T	: polymorphic base A or G	: polymorphic base A or G	polymorphic base A or G	: deletion of C	: polymorphic base C or T
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RESULT 9
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                                                         DB 4; Length 20674;
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Godfrey, Tony
APPLICANT: Kowbel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOURE: IBM PC compatible
COMPOURE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: BASTLAN, Kevin L.
REGISTRATION NUMBER: 023070-068900US
TELECOMMUNICATION INFORMATION:
                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                            0; Mismatches
                                                     Score 19.2;
Pred. No. 16;
                                                                                                                                                   DD 13044 AAATGGTGGGCGGGGGGGGAGAC 13067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 1015 TAAAGGGGTGGGAGGAGGAGAC 991
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                                                                                                                                2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                            Sequence 4, Application US/08680395 Patent No. 5892010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                     Query Match 76.8%;
Best Local Similarity 87.5%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                       Gray, Joe W.
Collins, Colin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2605 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
NAME/KEY: allele
LOCATION: 13535
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US-08-680-395-4/c
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APPLICANT:
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RESULT 8

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Gaps
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APPLICANT: O'Hara, Bryan M.
TITLE OF INVENTION: Gibbon Ape Leukemia Virus Receptors
TITLE OF INVENTION: Gibbon Ape Leukemia Virus Receptors
TURBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products
STREET: One Campus Drive
CITY: Paralpapany
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIP: 06904-0060
COMPUTER READABLE FORM:
MEDUW TYER.
COMPUTER: IBM PC AT
COMPUTER: IBM PC AT
COMPUTER: ASCII CONVECTED IF TO THE 
                                                                        GENERAL INFORMATION:
APPLICANT:
Bryan Mark O'Hara
TITLE OF INVENTION: Gibbon Ape Leukemia
TITLE OF INVENTION: Virus Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: 1937 West Main Street
CITY: Stamford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.6; Di
Pred. No. 64;
0; Mismatches
Sequence 1, Application US/07674287B Patent No. 5414076
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Patent No. 5874264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 AAAAGGGAGGCGGAGAC 76
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 203 321 2361
TELEFAX: 203 321 2971
TELEX: 710 474 4059
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 3211 Base Pairs
TYPE: NUCLEOTIDE SEQUENCE
STRANDENESS: Single
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ilarity 83.3%;
Conservative
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Best Local Similarity
Matches 20; Conserv
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Gaps
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APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               Herpes simplex virus-1 b' 42K gene
(start site 106547)
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 50;
95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075,32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
INFORMATION FOR SEQ ID NO: 505:
SEQUENCE CHARACTERRIFICS:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
RELECOMMUNICATION NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 324-0860
TELEPHONE: (415) 324-0960
INFORMATION FOR SEQ ID NO: 505:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 68.0%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 95; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 505, Application US/08123936 Patent No. 5726014 GENERAL INFORMATION:
                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GIGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 GTGGGCGTGGGGGAGA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: 50 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                  ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-171-389-505
                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-123-936-505/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 3211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 505, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Sequence-Directed DNA Binding
WUMBER OF SEQUENCES: 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILLING DATE: 08-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                         CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,104-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AAAAGGGAGGCCGGAGGCGGGAGAC 76
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                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-436-900A-1
                                                                                                                                                                                                                                                          TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                  LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-171-389-505/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Red
STATE: CA
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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Gaps
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                  Herpes simplex virus-1 b' 42K gene (start site 106547)
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APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Trix E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
                                                                                                                 Length 50;
                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: RELOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: US/08/482,080A
FILING APPLICATION NUMBER: US 08/171,389
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING BATE: 17-SEP-1993
PRIOR RAPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING BATE: 23-DEC-1992
PRIOR RAPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING BATE: 23-DEC-1992
PRIOR RAPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING BATE: 27-JUN-1991
PRIOR RAPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING BATE: 22-JUN-1993
ATTONEY/AGENT INFORMATION:
NAME: RELAKE APPLICATION NUMBER: US 08/081,070
FILING BATE: 22-JUN-1993
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
                                                                                                               DB 2;
95;
                                                                                              68.0%; Sco.
100.0%; Pred. No. 5-,
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                   Sequence 505, Application US/08482080A Patent No. 6010849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (650) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                     Ouery Match
Best Local Similarity 100.
                                                                                                                                                                                                                                50 GTGGGCGGTGGGGGAGA 34
                                                                                                                                                                                                         8 GTGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                     ; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-475-228A-505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-482-080A-505/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
STATE:
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                                                                                                               Herpes simplex virus-1 b' 42K gene
(start site 106547)
                                                                                                                                                                                               68.0%; Score 17; DB 1; Length 50; 100.0%; Pred. No. 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 505, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Turin, Lisa M.
APPLICANT: Furin, Molecules, Compositions and Methods
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94063

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEO ID NO: 505:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-JUN-1995
PRIOR APPLICATION NUMBER: 08 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION NUMBER: US 07/996,783
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
FILING DATE: 27-JUN-1991
FILING DATE: 22-JUN-1991
FILING DATE: 22-JUN-1991
FILING DATE: 22-JUN-1991
FILING DATE: 22-JUN-1993
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                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Herpes s:
INDIVIDUAL ISOLATE: (start s)
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                                                                                                                                                                                                                                                                                              8 GTGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                      50 GTGGGCGGTGGGGGAGA 34
                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 505 Penobs/
CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                      Query Match
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              Herpes simplex virus-1 b' 42K gene (start site 106547)
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(start site 106547)
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                                                                                                                                                                                                                                                                                        FOT-US93-12388-505/c
| Sequence 505, Application PC/TUS9312388
| GENERAL INFORMATION:
| APPLICANT:
| TITLE OF INVENTION: Molecules, Compositions and Methods | NUMBER OF SEQUENCES: 641
| CORRESPONDENCE ADDRESS: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive
                                                                                            DB 4; Length 50;
95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                     Indels
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:

FILING DATE: 17-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US93/12388 FILING DATE:
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                                                                                                        100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 17;
100.0%; Pred. No.
Live 0; Mismatch
                                                                                            68.0%; Score 17; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signary Type: linear Type: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAN: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 505
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 GTGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 GTGGGCGGTGGGGGAGA 34
                                                                                            Query Match
Best Local Similarity 100.4
Matches 17; Conservative
                                                                                                                                                                                                 50 GTGGGCGGTGGGGGAGA 34
                                                                                                                                                                           8 GTGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
PCT-US93-12388-505
                INDIVIDUAL ISOLATE: INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE
                                                        US-09-354-947-505
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Herpes simplex virus-1 b' 42K gene (start site 106547)
                                                                                                                                                                                                                                                                                    Sequence 505 Application US/09354947

Patent No. 6384208

GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, KIrk E.
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
                                                                              Length 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/354,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKER NUMBER: 4600-0175.20/G19P3D1
TELEPHONE: (650) 324-0880
TELEPHONE: (650) 324-0960
INFORMATION FOR SEQ ID NO: 505:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                              DB 3;
95;
                                                                          68.0%; Score 17; DB 100.0%; Pred. No. 95; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
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APPLICATION NUMBER: US 08/482,080
FILING DATE: 07-070-1993
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-UN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-UN-1991
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-UN-1993
ATTORNEY AGENT INFORMATION:
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Matches 17; Conservative
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Search completed: January 19, 2003, 01:35:38 Job time : 52 secs

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1: /cgn2_6/ptodatca2/lna/5A_COMB.seq:*
2: /cgn2_6/ptodatca2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodatca/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodatca2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodatca2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodatca/2/lna/PcTUS_COMB.seq:*
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US-09-961-527-288
US-08-370-319C-12
US-09-724-84-12
US-09-770-319C-12
US-09-770-319C-12
US-09-770-319C-12
US-09-771-154-3
US-08-961-527-3
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US-08-961-527-3
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                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
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Perfect score:
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Fatent No. 6258788
GENERAL INFORMATION:
TITLE OF INVENTION: DNA VACCINES Against Tick-borne Flaviviruses
FILE REBERENCE: 003/00100/SAP RIID 96-10
CURRENT APPLICATION NUMBER: US/09/197,218A
CURRENT FILING DATE: 1998-11-20
FARLIER APPLICATION NUMBER: US 60/065,750
EARLIER FILING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 1
LENGTH: 2055
Sequence 5, Sequence 5, Sequence 3, Sequence 3, Sequence 1, Sequence 2, Sequence 5, Sequen
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PATEUR NO. 5486473

MANABE, SADAO; FUKAI, KONGONE

TITLE OF INVENTION: A DNA CODING FOR A FLAVIVIRUS ANTIGEN

NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/194,049

FILING DATE: 09-FEB-1994

PRIOR APPLICATION NUMBER: 809,255

FILING DATE: 18-DEC-1991

APPLICATION NUMBER: 279,685

FILING DATE: 05-DEC-1998

FILING DATE: 19-NOV-1986
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                     US-09-160-567-5
US-08-828-741B-3
US-09-160-567-3
US-09-328-111-124
US-09-328-111-124
US-09-165-868-4
5169941-2
US-08-570-923-1
US-08-570-923-1
US-09-079-785-1
US-09-079-785-1
US-09-016-000-10
US-09-289-466-1
US-09-016-000-10
US-09-160-10
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Pred. No. 6.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Central Buropean Encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-382-256-5
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us-09-674-593-9.rni

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Best Local Similarity
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; ORGANISM: Mus sp.
US-09-408-508-4
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US-08-961-527-167/c
                                      JS-09-408-508-4/c
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                                                                         Score 17.8; DB 6; Length 1491; Pred. No. 8.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Neuman, Toomas
APPLICANT: Suda, Kikuo
APPLICANT: Suda, Kikuo
TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN
TITLE OF INVENTION: NEURONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W.
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/362,495

FILING DATE: 18 "NOV-1996
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APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/14614
FILING DATE: 19-DEC-1994
PRIOR APPLICATION NUMBER: US 08/301,416
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/169,522
FILING DATE: 15-DEC-1993
ATTOWNEY/AGENT INFORMATION:
NAME: BATKET, M. PAUL
REGISTRATION NUMBER: 32,013
RECISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 05800.0001-020G
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 44000
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                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-362-495-4/c
'Sequence 4, Application US/08362495
'Patent No. 6087171
                                                                                                                                                                                                                                                                3 GGCTGTTTGGAAAGGGTAGCA 23
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                      Query Match 71.2%;
Best Local Similarity 90.5%;
Matches 19; Conservative (
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TYPE: nucleic acid
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Matches 20; Conserv
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ADDRESSEE:
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Sequence 167, Application US/08961527
Patent No. 6420135
PARENT NO. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
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                                                                                       APPLICANT: Suda, Kikuo

PEPLICANT: Suda, Kikuo

TITLE OF INVENTION: Method For Inducing DNA Synthesis in Neurons
FILE REFERENCE: 05800,0001-04

CURRENT APPLICATION NUMBER: US/09/408,508

PRIOR APPLICATION NUMBER: 08/362,495

PRIOR PILING DATE: 1996-11-18
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Pred. No. 22;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
COMPUTER: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                    68.0%; Scor.
80.0%; Pred. No. 22.
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Sequence 4, Application US/09408508
Patent No. 6372721
GENERAL INFORMATION:
APPLICANT: Neuman, Toomas
APPLICANT: Suda, Kikuo
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34C
TELECOMMUNICATION INFORMATION:
TELEFAM: (301) 309-8514
TELEFAM: (301) 309-8512
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 9711 base pairs
TYRHE: nucleic acid
STRANDEDRESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: ARLINGTON
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
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US-09-147-119-5
                                                                                                                                                                    COUNTRY:
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   DB 4; Length 9711;
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                                         Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION THEORER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTOMNEY/AGENT INFORMATION:
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Score 16.6; DE Fred. No. 53; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.8%; Score 16.2;
85.7%; Pred. No. 48;
                                                                                                                                                                                                                                                                            APPLICANT: Steiner, Sabine APPLICANT: Steiner, Sabine APPLICANT: Mont, Christine APPLICANT: Wendland, Jurgen APPLICANT: Knechtle, Philipp APPLICANT: Rebischung, Corinne TITLE OF INVENTION: GENOMIC DNA SEQUEN TITLE OF INVENTION: ADD USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                      Sequence 552, Application US/08998416 Patent No. 6239264
                                                                                            D 1972 TTGGCTTTTTGGGAATGGTAGCA 1950
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US-08-985-908-23
: Sequence 23, Application US/08985908
                                                                          1 TAGGCTGTTTGGAAAGGGTAGCA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 552: SEQUENCE CHARACTERISTICS: LENGTH: 849 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 CIGITIGAAIGGGIGGCACA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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 Ouery Match 66.4%;
Best Local Similarity 82.6%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: NO. 62392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27709
                                                                                                                                                                      RESULT 6
US-08-998-416-552
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APPLICANT: BAIER, Michael
APPLICANT: WERNER, Albrecht
TITLE OF INVENTION: GENOMIC UCLEIC ACIDS, CDNA AND MRNA WHICH
TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
Patent No. 6004773
GENERAL INFORMATION:
APPLICANT: MASAVUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSHI
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 1331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: MEDIUM TYPE:

MEDIUM SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAECHLIN Release #1.0, Version #1.30

SOFTWARE: PAECHLIN DATA:

APPLICATION NUMBER: US/08/985,908

FILING DATE: 05-DEC-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: JP 8-325659

FILING DATE: 05-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: NORMAN F. OBLON

REGISTRATION NUMBER: 24,618

TELECOMMUNICATION INFORMATION:

NAME: NORMAN F. OBLON

REGISTRATION NUMBER: MEDIUM TREILEDHUMINGATION:

NAME: NORMAN F. OBLON

TELEPHONE: APPLICATION INFORMATION:

THE PROFILE APPLICATION INFORMATION INFORMATION:

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85.7%; Pred. No. 54;
Live 0; Mismatches
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Patent No. 6338844
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 GCTGTTTGGTAAGGTAGCGC 272
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TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GCTGTTTGGAAAGGGTAGCAC 24
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ORIGINAL SOURCE:
ORGANISM: Escherichia col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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GENERAL INFORMATION:

APPLICANT: KURTH, Ruth
APPLICANT: BAIER, Michael
APPLICANT: BAINER, No. 6338844bert
APPLICANT: BANNER, No. 6338844bert
APPLICANT: METANER, Marin
APPLICANT: METANER, Marin
APPLICANT: METANER, Albrecht
TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, CDNA AND MRNA WHICH
TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Nikaido, Marmeistein, Murray & Oram LLP
STREET: 655 Fifteenth St., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,119
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PCT/EP97/01753
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 14 099.4
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: WONG, KING L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P1614-8068
TELECPOMUNICATION INFORMATION:
TELEPAX: (202) 638-5000
TELEPAX: (202) 638-5000
TELEPAX: (202) 638-5000
TELEPAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15936 base pairs
TYPE: nucleic acid
STRANDEDDESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FRATURE:
NAME/KEY: exon
LOCATION: 3100..3238
                                                                                                                                                      Sequence 1, Application US/09147119
Patent No. 6338844
                                         3132 GGCTGCGTGGAGAGGGTAGCA 3152
                     3 GGCTGTTTGGAAAGGGTAGCA 23
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12065..12323
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7504..7672
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5540..6635
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9711..9812
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US-09-147-119-1
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                   COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,119
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/EP97/01753
FILING DATE: 10-APR-1996
PRIOR APPLICATION NUMBER: DE 196 14 099.4
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: WONG, King L.
REGISTRATION NUMBER: P1614-8068
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (202) 638-600
TELEPHONE: (202) 638-601
TELEPHONE: (202) 638-610
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
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5484..5737
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2973..5224
ZIP: 20005-5701
COMPUTER READABLE FORM:
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7927..9096
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833..2870
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339..663
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LOCATION: 1..338
FEATURE:
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LOCATION:
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ST: 805 Third Avenue
New York City
S: New York
                                                                                             ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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OTHER INFORMATION:
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                USA
                                                                                                                                                                                10022
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STREET: 80
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                                                                                                                                                                                                                                                                          Sequence 288, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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APPLICANT: Traversari, Catia; W lfel, Thomas; Coulie, Pierre;
                                                                                                 DB 4; Length 15936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 540;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB /
55;
                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                 Score 16.2;
Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                         STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELEPHONE: (701) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/08370319C
Patent No. 5856091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AGGCTGTTGTGAAACGGTTGCAAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AGGCTGTTTGGAAAGGGTAGCACA 25
                                                                                                                                                                                9972 GGCTGCGTGGAGGGTAGCA 9992
                                                                                                                                                                23
                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 18; Conservative
                                                                                                                                                              3 GGCTGTTTGGAAAGGGTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 540 base pairs
nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.28
Matches 19; Conservative
                                exon
14767..15936
12578..12703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                              US-08-961-527-288/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-370-319C-12/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY:
US-08-961-527-288
LOCATION:
                              ; NAME/KEY:
; LOCATION:
US-09-147-119-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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TITLE OF INVESTION: ISOLATED WICKLER CARLD SEQUENCE COUNE FOR A TITLE OF INVESTION: ISOLATED WICKLER CARLD SEQUENCE COUNE OF FAILTE OF INVESTION: ISOLATED WICKLER CARLD SEQUENCE PROCESSED TO AT LEAST ONE TITLE OF INVESTION: TOWN NATIONS WITCHES PRECESSED TO AT LEAST ONE TITLE OF INVESTION: REPORT OF THE ANALYSE PROCESSED TO AT LEAST ONE TITLE OF INVESTION: REPORT OF THE ANALYSE PROCESSED TO AT LEAST ONE TITLE OF INVESTION: REPORT OF THE ANALYSE PROPERTY OF T
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Gaps

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DB 2; Length 4503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: IKEDA, JUN
APPLICANT: KANEDA, SUMIKO
APPLICANT: YANAGI, HIDEKI
APPLICANT: YURAA, TAKABHI
TILLE OF INVENTION: NOVEL STRESS PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEMART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLNG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

Query Match

Best Local Similarity 79.2%; Pred. No. 88;

Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION:

CLASSIFICATION DATA:

APPLICATION NUMBER:

FILING DATE: 20-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: MURPHY JR, GERALD M

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 1422-287

TELECHONE: (703)-205-8050

INFORMATION FOR EXPANDANCE TELECHONE: (703)-205-8050

INFORMATION FOR EXELID NO: 2:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERNICE/DOCKET NUMBER: 1422-287
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8050
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGHH 4503 base pairs
TYPE: nucleic adid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DD 1849 AGCCTGTTTGGAGGCGGTACCACA 1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGCTGTTTGGAAAGGGTAGCACA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09175581 Patent No. 6034232
                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
; IDENTIFICATION METHOD: E
US-08-770-301A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 4503 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-175-581-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence is preceded by an unsequenced portion of from 4.7 to 5.3 kilobases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coh 64.0%; Score 16; DB 4; Length 4129; 11 Similarity 79.2%; Pred. No. 86; 19; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22040-0747
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,301A
FILLNG DATE: 20-DEC-1996
CLASSIFICATION: 435
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08770301A

Patent No. 5948637

GENERAL INFORMATION:
APPLICANT: IKEDA, JUN
APPLICANT: RANEDA, JUN
APPLICANT: MATSUMOTO, MASAYASU
CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PELLING DATE: 18-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6201111man D.
REGISTRATION NUMBER: 30,946
REPERENGE/DOCKET NUMBER: LUD 5377.1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-3200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,319
                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/224,834
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             732 AGTCAGTTTGGAAAGTATACCACA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AGGCTGTTTGGAAAGGGTAGCACA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4129 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION:
CTHER INFORMATION:
CTHER INFORMATION:
US-09-224-834-12
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: FALL;
STATE: VA
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January 18, 2003, 23:44:49; Search time 57.5 Seconds (without alignments) 193.856 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                             393868 seqs, 222934149 residues
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25
1 taaatgggtgggcggtgggggagac
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

SUMMARIES

	Description	Sequence 1976, Ap	Sequence 72, App.	7, A	Sequence 5, Ap	Sequence 5830,	Sequence 670,	Sequence 4421,	Sequence 137, App	Sequence 356, A	Sequence 172, App	211,	Sequence 7, Appl	Sequence 312, App	Sequence 1960,	Sequence 2872,	Sequence 1, Appl	Sequence 1, Appl	ī	Sequence 19262
	ID	US-09-938-842A-1976	US-09-764-864-72	US-09-927-091-7	US-09-927-091-5	US-09-923-876-5830	US-09-728-446-670	US-09-878-574-4421	US-09-954-531-137	US-09-954-531-356	US-09-981-353-172	US-09-974-300-211	US-09-835-232-7	US-10-040-739-312	US-09-954-456-1960	US-09-880-107-2872	US-09-946-807-1	US-09-795-668-1	US-09-795-686-1	US-09-864-761-19262
	DB	6	10	10	10	10	10	10	6	6	6	10	10	6	10	10	6	10	10	10
	Duery Match Length DB	639	853	23433	30625	273	276	501	3220	3220	3290	345	170834	268	390	390	1503841	1503841	1503841	305
dЮ	Query Match	75.2	72.8	72.8	72.8	70.4	70.4	70.4	70.4	70.4	70.4	68.8	68.8	68.0	68.0	68.0	68.0	68.0	68.0	67.2
	Score	18.8	18.2	18.2	18.2	17.6	17.6	17.6	17.6	17.6	17.6	17.2	17.2	17	17	17	17	17	17	16.8
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Sequence 536, App	Sequence 2534, Ap	Sequence 3814, Ap	Sequence 9889, Ap	Sequence 20, Appl	Sequence 5580, Ap	Sequence 2, Appli	Sequence 99, Appl	Sequence 180, App	Sequence 3285, Ap	Sequence 2167, Ap	Sequence 12, Appl	Sequence 528, App	Sequence 1, Appli	Sequence 3189, Ap	Sequence 183, App	Sequence 183, App	Sequence 3, Appli	Sequence 19, Appl	Sequence 4, Appli	Sequence 251, App	Sequence 6, Appli	Sequence 3, Appli	Sequence 680, App	Sequence 3994, Ap	Sequence 36, Appl
US-09-563-817-536	US-09-864-761-2534	US-09-880-107-3814	US-09-960-352-9889	US-09-768-827-20	US-09-960-352-5580	US-09-728-628-2	US-09-822-849A-99	US-09-925-297-180	US-09-880-107-3285	US-09-880-107-2167	US-09-919-497-12	US-10-044-090-528	US-09-931-157-1	US-09-764-877-3189	US-09-853-526-183	US-09-901-484A-183	US-09-835-081-3	US-09-822-849A-19	US-09-878-262B-4	US-10-044-090-251	US-09-878-262B-6	US-09-804-472-3	US-09-933-797-680	US-09-923-876-3994	US-09-416-384A-36
10	10	10	10	თ	10	10	10	10	10	10	10	12	10	10	6	10	10	10	10	12	10	10	σ	10	10
463	496	198285	404	405	427	1095	1379	1827	2214	2523	2595	2901	4105	7739	37950	37950	57130	1364	1524	2466	2469	65329	208	286	455
7.2	7.2	7.2	6.4	6.4	6.4	6.4	66.4	4.9	4.9	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	9.9	5.6	9.6	5.6	9.9	4.8	4.8	4.8
9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	Ó	ف	ý
8.9	6.8	6.8	9.9	9.9	9.9	9.9	16.6	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	6.4	6.4	6.4	6.4	6.4	6.2	6.2	6.2
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20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45
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ALIGNMENTS

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Sequence 1976, Application US/09938842A

Sequence 1976, Application US/09938842A

Datent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US 60/224

PRIOR PLILING DATE: 2001-08-24

PRIOR PLILING DATE: 2000-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR PLILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.2%; Score 18.8; DB 9; 90.9%; Pred. No. 31; iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 72, Application US/09764864; Patent No. US2002013753A1
GENERAL INFORMATION: APPLICAWT: ROSen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AATGGGTGGGCGGTGGGGGAGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           634 AATGTGGGGAGGTGGGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.9
Matches 20; Conservative
RESULT 1
US-09-938-842A-1976/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-938-842A-1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-764-864-72/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
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70.4%; Score 17.6; D
83.3%; Pred. No. 90;
7ative 0; Mismatches
                                                                                                                                                                                                                                                                             Score 18.2; D
Pred. No. 64;
0; Mismatches
                                                                                                                                                                          NAME/KEY: modified_base;

! LOCATION: (4/54)...(30625)

OTHER INFORMATION: n = A or C or G or T/U

US-09-927-091-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: unsure

) LOCATION: 10, 44, 196

) CHER INFORMATION: a, t, c, g, or other

US-09-923-876-5830
      PRIOR APPLICATION NUMBER: 60/225,033 PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                             Db 16649 TACAGGGGTGGGAGGTGGGGGAG 16627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 AAATTGATGGGTGGTGGGCAGAC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                        1 TAAATGGGTGGGCGGTGGGGGAG 23
                                                                                                                                                                                                                                                                             Query Match 72.8%;
Best Local Similarity 87.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3.
                                          NUMBER OF SEQ ID NOS: 9 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-923-876-5830/c
                                                                                                                                         ORGANISM: Human
                                                                                                       30625
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US-09-728-446-670
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LENGTH: 273
                                                                                 SEQ ID NO 5
LENGTH: 3(
                                                                                                                         TYPE: DNA
                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                             Length 853;
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERBNCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 72
LENGTH: 853
                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: KILLARY, ANN
APPLICANT: LOTT, STEVE
APPLICANT: LOTT, STEVE
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
FILE REFERENCE: UTSC: 651US
CURRENT FILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-20
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-22
PRIOR FILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
SOFTWARE: PALCHIN VOWER: 60/225,033
PRIOR FILING DATE: 2000-08-10
SOFTWARE: PALCHIN VOR: 9
SOFTWARE: PALCHIN VOR: 2.1
SEQ 1D NO 7
LENGTH: 23433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KILLARY, ANN
APPLICANT: LOTT, STEVE
APPLICANT: CHANDLER, DAWN
TITLE OF INVENTION: THE TUMOR SUPPRESSOR CAR-1
FILE REFERENCE: UTSC:651US
CURRENT FILLING DATE: 2001-08-09
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                         Score 18.2; D
Pred. No. 55;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (5071)...(23433)
; OTHER INFORMATION: n = A or C or G or T/U
US-09-927-091-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAATGGGTGGCGGTGGGGGAGA 24
||| |||||||| || |||||| ||
608 AAAAGGGTGGGGGGGA 586
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; Patent No. US20020119541A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09927091
Patent No. US20020119541A1
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Best Local Similarity 87.0%;
Matches 20; Conservative
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                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-864-72
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Best Local Similarity
Matches 20; Conserva
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ORGANISM: Human
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US-09-927-091-7/c
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Sequence 5830, Application US/09923876

Sequence 5830, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNOCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT FILING DATE: 2001-08-06

PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 09/298,329

PRIOR APPLICATION NUMBER: 60/085,331

PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram
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Patent No. US20020081668A1

GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081668A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0101-USA
                                                   Gaps
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Length 30625;
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OTHER INFORMATION: Incyte ID No. US20020013958A1 700457813H1
                                                   Indels
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APPLICATION TO APPLICATION TO APPLICATION TO APPLICATION TO APPLICATE APPLICATION TO APPLICATE APPLICATION TO APPLICATE APPLICATION TO APPLICATE OF INVENTION TO Gene Sets TILE OF INVENTION Gene Sets TILE OF INVENTION Gene Sets TILE REFERENCE: 689290-77 CURRENT APPLICATION NUMBER: 0200-09-18 PRIOR APPLICATION NUMBER: 0560/234,009 PRIOR FILING DATE: 2000-09-18 PRIOR PLILING DATE: 2000-09-20 PRIOR PAPLICATION NUMBER: 05/60/234,009 PRIOR PLILING DATE: 2000-09-20 PRIOR PALICATION NUMBER: 05/60/234,509 PRIOR PALICATION NUMBER: 05/60/234,567 PRIOR APPLICATION NUMBER: 05/60/234,567 PRIOR APPLICATION NUMBER: 05/60/234,567 PRIOR PRILING DATE: 2000-09-22 PRIOR PLILING DATE: 2000-09-20 PRIOR PR
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APPLICANT: Lasek, Amy W.
APPLICANT: Lones, David A.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER FILE REFERENCE: PA-0038 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 356, Application US/09954531
; Patent No. US20020165180A1
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; Patent No. US20020160382A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 AAAAGGGAGGGCGGAGAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAATGGGTGGGCGGTGGGGGAGAC 25
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1 Similarity 83.3%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens US-09-954-531-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
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LENGTH: 3220
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LENGTH: 3220
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-77
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nocleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 4421
LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
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: LOCATION: (1)..(501)

: OTHER INFORMATION: unsure at all n locations

: OTHER INFORMATION: Clone ID: LIB3028-022-Q1-B1-C2

US-09-878-574-4421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.4%; Score 17.6; Best Local Similarity 83.3%; Pred. No. 90; Matches 20; Conservative 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/728,446
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,270
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 670
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4421, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
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Patent No. US20020165180A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 TAAATGGCCTGCCGGGGGGGA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TGAAGGGTGGGGGGAGA 386
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LCCATION: (1)...(276)
CTHER INFORMATION: n = A,T,C or G
US-09-728-446-670
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                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine max
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US-09-954-531-137/c
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Gaps

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Indels

Score 17.2; DB 10; Pred. No. 1.6e+02; 0; Mismatches 3;

Length 170834;

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NAME/KEY: misc_feature

LOCATION: (1)...(170834)

COTHER INFORMATION: n= A,T,C, or G

US-09-835-232-7
                                                                                                                                                                                                                                                          1 TAAATGGGTGGGCGGTGGGGGA 22
                                                                                                                                                                       68.8%;
86.4%;
                                                                                                                                                                       Query Match
Best Local Similarity 86.4;
Matches 19; Conservative
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                          ORGANISM: Homo sapiens
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Best Local Similarity
Matches 20; Conserv
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US-10-040-739-312/c
                                                  FEATURE:
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Fatent No. US20020098489A1
GENERAL INFORMATION:
APPLICANT: Leader, Philip
APPLICANT: Leader, Benjamin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/196,811
FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 345;
                                                                                                                                                                                                                                                                         Score 17.6; DB 9; Length 3290;
Pred. No. 1e+02;
0; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT BETAN RAND M.

APPLICANT Clausen, ID Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT FILINO BATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 06/279,526
PRIOR PLILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-10-06
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                       ) NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 2023119CB1
US-09-981-353-172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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86.4%; Pred. No. 1.3e+02;
tive 0; Mismatches 3;
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 211, Application US/09974300 Patent No. US20020146721A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    172 AAAAGGGAGGCGGAGAC 149
                                                                                                                                                                                                                                                                                                                                                            2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 345
7 TYPE: DNA
7: ORGANISM: Bacillus licheniformis
0S-09-974-300-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 AATGGGGGGGGGGGGGGA 249
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                                                                                                                                                                                                                                                                              70.4%;
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Best Local Similarity 83.39
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 19; Conservative
                                                                              SEQ ID NO 172
LENGTH: 3290
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-974-300-211/c
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LENGTH: 170834
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                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
COUNTRY: U.S.A
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OOMENTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/040,739
FILING DATE: 07-Jan-2002
CLASSIFICATION: CURKOWN>
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                                                                                                                                                                                                              EXPRESSED SEOUENCE TAGS
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llarity 80.0%; Pred. No. 1.6e+02;
Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-040-739-312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/036,520 FILING DATE: 03-JUN-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724
Sequence 312, Application US/10040739 Patent No. US20020173635A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                 McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 268 base pairs
                                                              APPLICANT: Jacobs, Kenneth
                                                                                                                                               Merberg, David
Treacy, Maurice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
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Gaps
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COTHER INFORMATION: Genbank Accession No. US20020142981A1 R48540
HAME/KEY: unsurvey: US20020142981A1 R48540
LOCATION: (1). (390)
OTHER INFORMATION: n = a or c or g or t
US-09-880-107-2872
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Job time : 100.5 secs
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LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                           Sequence 1960, Application US/09954456

Fatent No. US200201555A1

GENERAL INFORMATION:

APPLICANT: Young, Paul

TITLE OF INVENTION: Paccess for Identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Paccess for Identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Paccess for Identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TOTAL OF APPLICATION NUMBER: US/09/954,456

CURRENT APPLICATION NUMBER: US/09/954,456

FRIOR FILING DATE: 2000-09-18

FRIOR FILING DATE: 2000-09-25

FRIOR PAPLICATION NUMBER: US/09/235,134

FRIOR FILING DATE: 2000-09-25

FRIOR APPLICATION NUMBER: US/09/235,637

FRIOR APPLICATION NUMBER: US/09/235,711

FRIOR PELING DATE: 2000-09-26

FRIOR APPLICATION NUMBER: US/09/235,711

FRIOR APPLICATION NUMBER: US/09/235,711

FRIOR APPLICATION NUMBER: US/09/235,711

FRIOR PELING DATE: 2000-09-27

FRIOR PELING DATE: 2000-09-27

FRIOR PELING DATE: 2000-09-27

FRIOR PELING DATE: 2000-09-27

FRIOR FILING DATE
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORNE, DATCI T.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:

TITLE REFERENCE: 4421-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/217,054

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFWWARE: PATENTIN VEY: 2.1

SEQ ID NO 2872
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Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 5; Indels
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; OTHER INFORMATION: n=a,t,g or C
US-09-954-456-1960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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US-09-880-107-2872
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nbxb0045N

BGS60434 BG501674 BH058191 AQ329897 BMS62440

us-09-674-593-8.rst

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BM833169 486 bp mRNA linear EST 06-MAR-2002
K-EST0107772 S5SNU484s1 Homo sapiens cDNA clone S5SNU484s1-12-C04
                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 486)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
Korea Hesenrch Institute of Bioscience & Biotechnology
Fel: +82-42-860-4470
Fax: +82-42-866-4409
                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: yongsung@mail.kribb.re.kr
Plate: 12 row: C column: 04
High quality sequence stop: 486.
Location/Qualiflers
                                                                                                                      BIO69548
BIO70677
AG184729
AV552048
AQ067630
AV543385
CNS026L8
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AV548307
AV546087
AV547147
      BE283772
BB277121
BG860434
BG501674
BH058191
                                                    CNS0397K
BM882409
BH477324
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AV545806
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AV541495
AV544358
AV545075
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BE973172
                                                                                            CNS02P0Z
BQ219869
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BI070676
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5', mRNA sequence.
BM833169
                                                                                            human.
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KEYWORDS
SOURCE
ORGANISM
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BM833169/c
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AUTHORS
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BG749180 602708139
BQ953400 AGENCOURT
                                            January 18, 2003, 23:34:34; Search time 1569 Seconds (without alignments) 258.054 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                   32308132
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                  Potal number of hits satisfying chosen parameters:
                                                                                                                      16154066 segs, 8097743376 residues
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                                                                                    1 taaatgggtgggcggtggggagac
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Maximum Match 100%
Listing first 45 summaries
                                OM nucleic - nucleic search, using sw model
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BQ650550
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Searched:

Minimum Maximum

AL233561 Tetraodon BM882409 Tetraodon BH47324 BOHONGOTF BH4773172 601651873 BH661879 BOMING2TR BE973172 60165185 AL207404 Tetraodon BE973172 60165186 AL207404 Tetraodon B1070676 C042P150 B1065548 C003P020 B1070676 C042P160 AL352875 Tetraodon B1070676 C042P160 AL35287 C042P160 AG184729 Pan trogl AV552048 AV552048 AV543185 AV543799 AV543185 AV543799 AV543185 AV543795 AV545806 AV543795 AV546087 AV546682 AV544683 AV546825 AV5446438 AV544358 AV5446438 AV544358 AV5446438 AV546682 AV544688

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Location/Qualifiers
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                             /docto="Organ: Stopanowach; Vector: pT218RP1; Site_1: ECORI;
Site_2: Not1; The poly (A)+ RNA was decapped with tabacco acid pyrophosphatase (TAP) and ligated with bna-RNA linker including EcoRI site by treatment of T4 RNA ligase. The first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOf' by electroporation method. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blotinylated single stranded RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuse, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. Coli ToplOfF' with a constructed by
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Frourement: ATCC

CDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

CDNA Library Arrayed by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llni.gov

Plate: LLCM2558 row: j column: 03

High quality sequence stop: 534.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 845)
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                                                    /clone="S5SNU484s1-12-C04"
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                                                                                                                                                           cell_type="Epithelial"
cell_line="SNU-484"
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                                                                          /clone_lib-"S5SNU484s1"
                                                                                                                                  /tissue_type="Stomach"
                        'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 g
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BQ948660
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Best Local Similarity
Matches 25; Conserva
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JOURNAL
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inxace:6286493"
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/lab_host="DH10B (phage-resistant)"
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ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size into Ecority costructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript in RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                              /clone_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle_inver.ergingle
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5/.mRNA sequence.
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CaAP (Stanford)

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCMA487 row: g column: 06

High quality sequence stop: 667.

Location/Qualifiers

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1. 898
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
                                                                                                          /clone="IMAGE:6376418"
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BG749180.1 GI:14059833
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/lab_host="bH10B (phage-resistant)"
/note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oliqo-dT priming Directionally cloned
into ECORI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                               BQ650598 963 bp mRNA linear EST 15-JUL-2002 AGENCOURT_8207577 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6283187
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BG749180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.go.
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.lln.gov
Plate: LLCM2478 row: m column: 12
High quality sequence stop: 618.
I. 963
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NIH-WGC http://mgc.nci.nih.gov/.
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Pred. No. 55;
Mismatches 0; Indels
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/clone_lib="NIH_MGC_100"
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BQ650598
BQ650598.1 GI:21774770
                                 100.0%;
100.0%;
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                        Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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Matches 25; Conserv
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KEYWORDS
SOURCE
ORGANISM
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BQ650598/c
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AUTHORS
TITLE
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BG749180
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BQ953400 879 bp mRNA linear EST 21-AUG-2002 AGENCOURT_8784199 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6376296
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Memaalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1045)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Contact: Robert Strausberg, Ph.D.

Email: capabs-rfemail.nih.gov

Tissue Procurement: Arrayed by: The I.M.A.G.E. Consatory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 09
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Pred. No. 55;
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/db_xref="taxon:9606"
/clone="IMAGE:4844744"
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Location/Qualifiers
1. .1045
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BQ953400
BQ953400.1 GI:22368878
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Gaps

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Pred. No. 1.8e+03;
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                                                                                             259 AATGGGTGGGAGGTGGGGGAGA 238
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                   95.58;
                                                                           3 AATGGGTGGGCGGTGGGGGAGA
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Best Local Similarity 88.0%
Matches 22; Conservative
                                   21; Conservative
                                                                                                                                                                                                                                                     mRNA sequence.
BE283772
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                   Best Local Similarity
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BE283772
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                                                                                                                                                                 /Library Library (2.2)
/(Library Library (2.2)
/(Library Library (2.2)
/(Library Library Constructed by Library Constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library | 1 others
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Site_1: EcoR1: Site_2: XhoI; total RNA extraction from
NaCl(200mm) treated Thellungiella salsugimea by RNAgent
Kit(Promega); mRNA isolation by MESSAGEMAKER Kit(GIECO BRL
); directional cDNA synthesis(EcoRI XhoI) by cDNA
Synthesis Kit(STRATAGEN); the ZAP express library by
GigapackII Gold Cloning Kit(STRATAGENE)"
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Wang, Z.L., Li, P. H., Sun, Y. F., Zhang, Q., Zhao, Y. X. and Zhang, H. Expressed sequence tags from a halophyte Thellungiella salsuginea
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/clone_lib="Thellungiella salsuginea ZAP cDNA library"
/dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library
Unpublished (2000)
Contact: Hui Zhang
Key Laboratory of Plant Stress Research
The Biology Department of Shandong Normal University
No.88, Wenhua East Road, Jinan, Shandong Province, 250014, PRC
Tel: (86)531-2960854
Email: Zhangheschu.edu.cn.
Location/Oualifiers
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BQ091950
BQ091950.1 GI:20072593
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                                                                                                                                                                                                                                                                                                                                                                                                                                          96.0%; Score 24; ·DB 14; I
100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
                 http://image.llnl.gov
Plate: LLCMX558 row: e column: 01
High quality sequence stop: 690.
Location/Qualifiers
                                                                                                                 /organism="Homo sapiens"
                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:6376296"
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Matches 2
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AUTHORS
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BE283772 910 bp mRNA linear EST 26-OCT-2000 601104026F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3501247 5',
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Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Musmanalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 910)
NIH-MGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Emall. ogapbs-r@mall.nih.gov
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LENL)
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88.0%; Pred. No. 2.2e+03;
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Indels

Pred. No. 2.9e+03;); Mismatches 2;

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2 AAATGGGTGGCCGGTGGGGGAGA 24
  Best Local Similarity 91.3
Matches 21; Conservative
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                               L. (Dades 1 to 233)

Konno, H., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Haroane, T., Horl, F., 1shi, Y., Hara, A., Hayatsu, N., Izawa, M., Kadota, K., Kagawa, T., Shikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Matsup, Y., Makamura, M., Oda, H., Okazaki, Y., Matsuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sugahara, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takhashi, F., Tominaga, N., Toya, T., Taunoda, Y., Watahiki, A., Yokota, T., Yoshida, K., Yoshiho, W., Muramatsu, M. and Hayashizaki, Y.

Unpublished (2000)

Contact: Yoshihde Hayashizaki, Y.

In Indocatory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9212
Fax: 81-45-503-9212
Fax: 81-45-503-9212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resegac.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Scl. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunah,Y., Akiyama,J., Shibata,K., Izawa,M., Rawai,J.,
Y. and Hayashizaki,Y., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/db_xref="taxon:10090"
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79.2%; Score 19.8; DB 10; Length 253;

Query Match

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/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhOI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAPP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5') and XhOI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
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                                                                                                                                              BG860434 10-29-MAY-2001 1024070F01.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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Duke University
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120 AAATGGGTGGGGGTTGGGGGAGA 98
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                                                                                                                                                                                                                                                                    BG860434.1 GI:14241618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG501674.1 GI:13463191
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Tel: 919 613 8159
Fax: 919 613 8177
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The Institute for Genomic Research
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El (bases 1 to 681)

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Right quality sequence stop; 618.
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Bukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 690)

Norman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,

Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,

Russell, D., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other_GSSS; RPCI-24-326E24.TV
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Pred. No. 3e+03;
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Department of Eukaryotic Genomics
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ilarity 91.3%;
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/db_xref="Exaon:10090"
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Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrharcoideae; Oryzaee; Oryza.

1 (bases 1 to 738)

Wing, R.A. and Dean, R.A.

A BAG End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                         end
                                                                                                              Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/Pacpac/orderingframe.htm). BAC e
page: http://www.tigr.org/tdb/Dac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
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9712 Medical Center Dr., Rockville, MD 20850, Tel: 301 838 0200
Fax: 301 838 0208
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Pred. No. 3e+03;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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AQ329897.1 GI:4121747
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91.38;
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Best Local Similarity 91.3
Matches 21; Conservative
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                                                                                                                                                              and subtropics, rely on rice as their primary curplication and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents The deep coverage allows the isolation a particular sequence with a probability of 99.9%. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening.
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/clone_lib="NIH MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/tab_host="bulb (phage=resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECRI; cobM made by voligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BM562440 896 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6597440 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5480956
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM2004 row: k column: 05
High quality sequence stop: 240.
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11H-MG http://mgc.ncl.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                         /lab_nost="E. coli DH10B"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
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/clone_lib="CUGI Rice BAC Library'
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BM562440.1 GI:18808533
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 006L12 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.

1 (bases 1 to 926)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 926)
Sost.Collius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                       896;
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/clone="006112"
/clone_lib="G"
                                                                                                                                                                                     Score 19.8; DB 13;
Pred. No. 3e+03;
0; Mismatches 2;
                                                                                                        166 t
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                                                                            NIH_MGC Library
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1 Similarity 91.3%;
21; Conservative
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Search completed: January 19, 2003, 01:33:49 Job time : 1572 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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January 18, 2003, 23:06:14; Search time 1670 Seconds (without alignments) 435.671 Million cell updates/sec 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues US-09-674-593-9 25 1 taggctgtttggaaagggtagcaca 25 OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapor 1.0 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:* em_htgo_hum:* em_htgo_mus:*

em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIE		AF181722	AF 161/20	AL359713	AC099072		TENSIYOR	TEN31958	TEN31958			AF091007											A02208	A02209	A48220	A57313		TEU2749				AC115853	AC027539	AP003460	AC00011/6	AC105849	AC105640	AC102207	AC023997	ALIGNMENT			1382 DP (RU2) mRNA, (531		
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Eukaryotza, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 1382)

Van Den Eynde, B.J., Gaugler, B., Probst-Kepper, M., Michaux, L., Devuyst, O., Lorge, F., Weynants, P. and Boon, T.

A new antigen recognized by cytolytic T lymphocytes on a human REFERENCE AUTHORS TITLE

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858 c 828 g 1380 t 15 others
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Homo sapiens chromosome 6 clone RP1-282H10 map p22.1-22.3, ***
SEQUENCING IN PROGRESS ***, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 120029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequesf@sanger.ac.uk on Jun 12, 2001 this sequence version replaced g1:12331282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4377;
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Sequencing vector: M13; M74815; 08 of reads
Sequencing vector: plasmid; L08752; 99 of reads
Sequencing vector: plasmid; L08752; 99 of reads
Chemistry: Dye-terminator ABI; 18 of reads
Chemistry: Dye-terminator Big Dye; 98% of reads
Consensus quality: 118224 bases at least 040
Consensus quality: 118634 bases at least 020
Insert size: 119629; sum-of-contigs
Insert size: 117431; 9.3% error; agarose-fp
Quality coverage: 18.41x in Q20 bases; sum-of-contig
coverage: 19.36x in Q20 bases; agarose-fp
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Pred. No. 0.083;
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AL132672.14 GI:14348905
HTG; HTGS_PHASE1; HTGS_CANCELLED.
                                             complement(1912. .2166)
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Best Local Similarity 100.0%;
Matches 25; Conservative 0;
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Direct Submission
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373 C 344 g 310 t
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Van Den Eynde, B. J., Gaugler, B., Probst-Kepper, M., Michaux, L., Devuyst, O., Lorge, F., Weynants, P. and Boon, T. A new antigen recognized by cytolytic T lymphocytes on a human kidney tumor results from reverse strand transcription J. Exp. Med. 190 (12), 1793-1800 (1999)
                                                                               2 (bases 1 to 1382)
Van den Eynde, B. J., Gaugler, B. and Pilotte, L.
Direct Submission
Direct Submission
Direct Submission
Avenue Hippocrate, 74, Brussels 1200, Belgium
Location/Qualifiers
1. 1382
/ Organism="Homo sapiens"
/ Chromosome="fe"
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/ Map="fe"
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/ Map="fe"
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Van den Eynde, B.J., Gaugler, B. and Pilotte, L.
Direct Submission
Submitted (30.*AG1999) Ludwig Institute for Cancer Research,
Avenue Hippocrate, 74, Brussels 1200, Belgium
Location/Qualifiers
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kidney tumor results from reverse strand transcription
J. Exp. Med. 190 (12), 1793-1800 (1999)
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738. .992
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Submitted (01-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UW. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On May 3, 2001 this sequence version replaced gi:13446455.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
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Human DNA sequence from clone RP11-95P3 on chromosome 6, complete
sequence.
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Kimborley,A.
Direct Submission
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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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0.065;
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102467. 120029
/note="assembly_fragment:02341

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    /note="assembly_fragment:05837
clone_end:SP6

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24840 c 24637 g 33666 t
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s; Pred. No. 0.06
0; Mismatches
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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                                                                                                                                                                                                                                                                               FEATURES
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only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, GANISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                           http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group.

Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RPI1-55P3 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-95P3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-95P3 is at 1 in this sequence. The true left end of clone RP1-73M23 is at 152867 in this sequence. The true right end of clone RP11-40E20 is at 17700 in this sequence.
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/hote-^AluJo/FRAM repeat: matches 181. .298 of consensus"
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6367. .6515
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5024. .5477
/note="LiM1 repeat: matches 1012. .1598 of consensus"
5581. .5859
/note="AluSg repeat: matches 18. .294 of consensus"
5986. .6359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6367. .6515
/note="FLAM_C repeat: matches 1. .143 of consensus"
6971. .7198
/note="L2 repeat: matches 1512. .1735 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2741 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2264. 2575
/note="AluSq repeat: matches 1. .311 of consensus"
3014. .3296
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note="MIR repeat: matches 65. .262 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521. 582
/note="L2 repeat: matches 2683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_11h="RPCI-11.1"
19. :544
10ote="match: GSS: Em:AZ517849"
24. :379
/note="match: GSS: Em:B63526"
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/note="match: GSS: Em:AQ315706"
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/note="match: GSS: Em:AQ285817"
10311, .10437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70. .589
/note="match: GSS: Em:AQ285677"
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/note="match: GSS: Em:B54691"
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/chromosome="6"
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// Nucle="macch: uso: mi:Ayzonovso.
complement(1970. .19546)
// Note="match: GSS: Em:A0128461"
| 19566. .19739
| 19566. .19739
| 19760. .20100
| // Note="LIMD3 repeat: matches 126. .295 of consensus"
| 19740. .20100
| // Note="LIMD3 repeat: matches 7391. .7739 of consensus"
| 121121. .21429
| // Note="AluJo repeat: matches 1. .310 of consensus"
| // Note="AluJo repeat: matches 1. .310 of consensus"
| // Note="AluJo repeat: matches 1. .310 of consensus"
| // Note="AluJo repeat: matches 1. .310 of consensus"
| // Note="10" copies 2 mer aa 60% conserved"
| // Note="10" copies 4 mer aaag 80% conserved"
| // Note="10" copies 4 mer aaag 93% conserved"
| // Note="10" copies 4 mer aagg 93% conserved"
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/note="AluJb repeat: matches 163. .299 of consensus" 28701. .28930
/note="Mill3 repeat: matches 32. .301 of consensus" 29080. .29171
'note="L2 repeat: matches 2612. .2747 of consensus"
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                              .309 of consensus"
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/note="Li2 repeat: matches 2580. .2.23980. .24292
/note="Alusq repeat: matches 2. .3
complement(27208. .27677)
/note="match: GSS: Em:AQ702871"
                               repeat: matches 1.
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complement(19337. .19501)
/note="match: GSS: Em:AQ268095"
              10710. .11022
/note="AluJo re
12006. .12156
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E l (bases 1 to 147525)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alicoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbario, J., Benton, J., Blange, K., Blankenburg, K., Bonnin, D., Burbario, J., Benton, J., Burnet, C., Burell, K.L., Byrd, N.C., Carch, P., C., Burch, D., Burkett, C., Burell, K.L., Byrd, N.C., Carcon, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.C., Denn, A.L., Ding, Y., Dinh, H.H., David, M.C., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Garner, T., Garza, N., Gall, R., Garner, T., Garza, N., Gall, R., Haris, C., Harris, K., Holloway, C., Hollins, B.,
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                      ion 30919. 31207)

// note="match: STS: Em:HS1J17"

// note="match: STS: Em:HS1J17"

// note="MIRSBA repeat: matches 1. .208 of consensus"

// note="MIRSBA repeat: matches 1. .371 of consensus"

// note="MIR repeat: matches 1. .371 of consensus"

// note="MIR repeat: matches 98. .250 of consensus"

// note="MIR repeat: matches 1. .297 of consensus"

// note="Alux repeat: matches 1. .297 of consensus"

// note="Alux repeat: matches 1. .297 of consensus"

// note="MIR repeat: matches 1. .297 of consensus"

// note="MIR repeat: matches 120. .232 of consensus"

// notes="MIR repeat: matches 120. .232 of consensus"
/note="MLT1H repeat: matches 433. .526 of consensus"
                          /note="L2 repeat: matches 2342, .2501 of consensus" 37251, .37544 /note="AluSx repeat: matches 1, .294 of consensus" 38446, .38493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="1.2 repeat: matches 1836. .1959 of consensus" 35164. .3461
/note="AluSq repeat: matches 2. .298 of consensus" 35532. .35990
/note="1.2 repeat: matches 2254. .2710 of consensus" 3631. .36790
/note="1.2 repeat: matches 2342. .2501 of consensus"
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38467. .38492
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Rodentia;
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Rattus norvegicus
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
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Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlson, E., Khan, U., Knay, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L. Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Liu, M., Mapua, P., Martin, R., Mar, J., Martines, E., Mawhiney, E., McLeod, M. P., Meador, M. Matther, E., Mawhiney, E., McLeod, M. P., Meador, M., McKeker, M., Maner, G., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Okwion, G., Mickerson, E., Nowcenko, S., Oguh, M., Okwion, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pinkens, R., Put. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Primus, E., Put. L., Quiles, M., Ren, Y., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergen, E., Soalke, T., Sparks, A., Stenley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Wardington, S., Ward-Moore, S., Warren, R., Washington, C., Wallilams, G., Williamson, A., Walshington, C., Warlington, S., Warley, W., Wall, W.Y., Wu, Y., Wu, Y., Washington, C., Wallington, S., Weinstock, G. and Gibbs, R., Dupublished
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Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA

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St Worley, K.C.

Direct Submission

L. Submitted (11-UTL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, Tx 77030, USA

On Jul 10, 2002 this sequence version replaced gi:17957215.
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NOTE: This is a "working draft' sequence. It currently consists of 59 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequenciary Statistics
Sequenciary vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 85085 bases at least Q40
Consensus quality: 93184 bases at least Q30
Consensus quality: 100226 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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KKGIEKLTVIGEHAMDFGSAGGFLSSIGKAV"
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Flavivirus; tick-borne encephalitis virus group.
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Characterization of tick-borne encephalitis virus from Latvia:
evidence for co-circulation of three distinct subtypes
J. Med. Virol. 65 (4), 730-735 (2001)
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Submitted (22-MAY-2001) Plyusnin A., Department of Virology,
University of Helsinki, Haartman institute, Haartmaninkatu 3, P.O.
Box 21, FIN-00014, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E gene for envelope protein,
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/organism="Tick-borne encephalitis virus"

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/lab_host="suckling white mice"
/country="Latvia"
1. .1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                TECK-borne encephalitis virus partial genomic RNA, strain Latvia-8110.
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/db_xref="G1:18076915"
                                                                                                                                                                                                              /product="envelope protein"
/evidence=experimental
                                                                                                                                                                                                                                                                                                                   0; Mismatches
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/isolate="Latvia-8110"
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AJ319583.1 GI:18076916
E gene, envelope protein.
Tick-borne encephalitis virus.
Tick-borne encephalitis virus.
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Best Local Similarity 91.3%;
Matches 21; Conservative
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/gene="E"
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Plyusnin, A.
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Tick-borne encephalitis virus.
Tick-borne encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Kalnina,V. and Plyusnin.A.
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evidence for co-circulation of three distinct subtypes
J. Med. Virol. 65 (4), 730-735 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-MAX-2001) Plyusnin A., Department of Virology, University of Helsinki, Haartman institute, Haartmaninkatu 3, P.O. Box 21, FIN-00014, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEN319582 1270 bp RNA linear VRL 08-APR-200 Tick-borne encephalitis virus partial E gene for envelope protein, genomic_RNA, strain Latvia-11686.
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/organism="Tick-borne encephalitis virus"
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/db_xref="taxon:11084"
/lab_host="suckling white mice"
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Pred. No. 14;
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AJ319582.1 GI:18076914
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95.5%;
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/gene="E"
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21; Conservative
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SPDVNVAMLITPNPTIENNGGGFIEMQLPPGDNIIYVGELSHQWFQKGSSIGRVFQKT
VKAACEAKKKATGHVYDANKIVYTVKVEPHTGDYVAANETHSGRKTASFTVSSEKTIL
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Flavivirus; tick-borne encephalitis virus group.
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Characterization of tick-borne encephalitis virus from Latvia:
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Submitted (22-Mar-2001) Plyusnin A., Department of Virology,
University of Helsinki, Haartman institute, Haartmaninkatu 3, P.O.
Box 21, FIN 00014, FINAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tick-borne encephalitis virus partial E gene for envelope protein, genomic RNA, strain Latvia-8369.
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/db_xref-"taxon:11084"
/lab_host-"suckling white mice"
/country-"Latvia"
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/evidence=experimental
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E gene; envelope protein.
Tick-borne encephalitis virus.
Tick-borne encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Tick-borne encephalitis virus partial E gene for envelope protein,
AJ319585
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Characterization of tick-borne encephalitis virus from Latvia:
evidence for co-circulation of three distinct subtypes
J. Med. Virol. 65 (4), 730-735 (2001)
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/lab_host="suckling white
/country="Latvia"
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/organism="Tick-borne
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/evidence=experimental
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Best Local Similarity 91.3%;
Matches 21; Conservative
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Plyusnin, A.
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Tick-borne encephalitis virus.
Tick-borne encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Tick-borne encephalitis virus.
Tick-borne encephalitis virus
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AJ319586.1 GI:18076922
E gene; envelope protein.
Tick-borne encephalitis virus.
Tick-borne encephalitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; tick-borne encephalitis virus
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EVGLEKLKMKGLTTYMCDKTKFTWRAAPTOSGHDTVVMEVTEGTKFCRIPKRAVAHG
SPDVNVAMLITPNPTIENNGGGFIEMQLPPGDNIIYVGELSHOWFQKGSSIGRRVPGYT
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Submitted (22-MAY-2001) Plyusnin A., Department of Virology,
University of Helsinki, Haartman institute, Haartmaninkatu 3, P.O.
Box 21, FIN-00014, FINAND
Location/Qualifiers
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Characterization of tick-borne encephalitis virus from Latvia: evidence for co-circulation of three distinct subtypes J. Med. Virol. 65 (4), 730-735 (2001)
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/db_xref="taxon:11084"
/db_host="suckling white mice"
/country="Latvia"
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/evidence=experimental
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21; Conservative
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Plyusnin, A.
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1488 bp RNA linear VRL 01-OCT-1998 Tick-borne encephalitis virus strain Absettarov polyprotein gene, AF091005
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YCLHARLSDTKVAARCPTWGPATLAEEHQGGTVCKRDQSDRGWGNHGCLFGKGSIVAC
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QNWNNAERLVEFGAPHAVKMDVYNLGDQTGVLLKALAGVPVAHIEGTKYHLKSGHVTC
SPDVWVAMLITPNPTLENNGGGFIEWQLEPGSGHTVVWEVTFSGTKPCRIPVRANG
KKGIERLTVIGEHAWDFGSAGGFLSSIGKAV"
VRL 04-JAN-2002
                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus; tick-borne encephalitis virus group.
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Submitted (05-OCT-2001) Plyusnin A., Department of Virology,
University of Helsinki, Haartman institute, Haartmaninkatu 3
Box 21, FIN-00014, FINLAND
                              E-gene for envelope
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/strain="Lithuania-262"
/db_xref="taxon:11084"
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Tick-borne encephalitis virus from Lithuania
Eur. J. Clin. Microbiol. Infect. Dis.
2 (bases 1 to 1270)
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1 Similarity 91.3%; Pred. No. 41;
21; Conservative 0; Mismatches 2:
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                        Tick-borne encephalitis virus partial glycoprotein, genomic RNA. AJ414703
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Query Match
Best Local Similarity 91.3%;
Matches 21; Conservative
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WFNDLALPWKHEGAQWWNNABRLVEFGAPHAVKMDVYNLGDOTGVLLKALAGVPVAHI
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/translation="SRCTHEN"
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1 (bases I to 1488)
Ecker, M., Allison, S.L., Meixner, T. and Heinz, F.X.
Sequence analysis and genetic classification of tick-borne encephalitis viruses from Europe and Asia
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Unpublished
Chases 1 to 1488)
Ecker,w. Allison,S.L., Meixner,T. and Heinz,F.X.
Direct Submission
Submitted (11-SEP-1998) Institute of Virology, University of Vienna, Kinderspitalgasse 15, Vienna 1095, Austria
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Tick-borne encephalitis virus strain Als. I polyprotein gene,
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Submitted (11-SEP-1998) Institute of Virology, University of
Vienna, Kinderspitalgasse 15, Vienna 1095, Austria
Location/Qualifiers
Flavivirus; tick-borne encephalitis virus group.

1 (bases 1 to 1488)

Ecker,M., Allison,S.L., Meixner,T. and Heinz,F.X.
Sequence analysis and genetic classification of tick-borne encephalitis viruses from Europe and Asia
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/strain="Als. I"
/db_xref-"taxon:11084"
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/strain="Absettarov; Abs"
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Ecker, M., Allison, S.L., Meixner, T. and Heinz, F.X.
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/note="E"
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Tick-borne encephalitis virus
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Arvylu09 1488 bp RNA linear VRL 01-OCT-1998
Tick-borne encephalitis virus strain Iso 40 polyprotein gene,
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Tick-borne encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Flavivirus; tick-borne encephalitis virus group.

[ (bases 1 to 1488)
Ecker, M., Allison, S.L., Meixner, T. and Heinz, F.X.
Sequence analysis and genetic classification of tick-borne encephalitis viruses from Europe and Asia
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NHCGLFGKGSIVACVKAACEAKKKATGHVYDANKIVYTVKVEPHTGDYVAANETHSGR
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2 (bases 1 to 1488)
Ecker,M., Allison,S.L., Meixner,T. and Heinz,F.X.
Direct Submission
Submitted (11-SEP-1998) Institute of Virology, University of Vienna, Kinderspitalgasse 15, Vienna 1095, Austria
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FORGSSIGRYFQKTKGIERLTV1GBHAWDFGSAGGFISSIGKAVHTVLGGAFNSIFG
GVGFLLLGVALAWLGLNMRNPTMSMSFLLAGGLVLAMTLGVGAFNSIFG
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Tick-borne encephalitis virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
I bases I to 1488)
Ecker,M., Allison,S.L., Meixner,T. and Heinz,F.X.
Sequence analysis and genetic classification of tick-borne encephalitis viruses from Europe and Asia
                                                                                                                                                                                                                                                                   AF091010 1488 bp RNA linear VRL 01-0CT-1998
Tick-borne encephalitis virus strain K23 polyprotein gene, partial
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Ecker M. Allison.S.L., Meixner,T. and Heinz,F.X.
Direct Submission
Submitted (11-SEP-1998) Institute of Virology, University of Vienna, Kinderspitalgasse 15, Vienna 1095, Austria
1. 1488
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                                      Length 1488;
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/strain="K23"
/db_xref="taxon:11084"
                                                                                 Indels
                                      Score 19.8; DB 14;
Pred. No. 41;
0; Mismatches 2;
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91.3%;
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                                    Query Match
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SOURCE
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AUTHORS
TITLE
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AUTHORS
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AF091010
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GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: January 18, 2003, 23:44:49; Search time 57.5 Seconds

(without alignments)
193.856 Million cell updates/sec

Title: US-09-674-593-9

Perfect score: 25
Sequence: 1 taggctgtttggaaagggtagcaca 25
Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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Published_Applications_NA:*

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14: /cgn2_6/ptodata/1/pubpna/VS60_PUBCOMB.seq:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Ouery Score Match Length DB 18.2 72.8 731 10 18.2 72.0 372 10 18 72.0 372 10 18 72.0 372 10 18 72.0 372 10 17.6 70.4 3690 9 17.6 70.4 3690 9 17.6 70.4 3690 9 17.6 70.4 3690 9 17.6 70.4 3690 9 17.6 66.4 3620 10 16.6 66.4 362 10 16.6 66.4 1500 9 16.5 66.4 1500 9 16.5 66.4 1500 9 16.2 64.8 231 9 16.2 64.8 231 9 16.2 64.8 231 9
SCORE 18.2 18.2 18.2 17.6 17.6 17.6 16.6 16.6 16.2 16.2
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NOT 1010 1010 1010 1010 1010 1010 1010 10
Result 0 100. 0 100. 0 100. 0 100. 0 100. 0 100. 0 100. 0 100. 0 100. 0 100. 0 100.

Sequence 392, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76

Sequence 31909, A Sequence 188, App Sequence 1182, App Sequence 11427, A Sequence 11427, A Sequence 55, Appl Sequence 616, App Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence 134, Appl Sequence 53, Appl Sequence 53, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 610, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 54, Appl Sequence 33, Appl Sequence 33, Appl Sequence 670, Appl Sequence 695, A	id and Protein Homologs	Length 731; Indels 0; Gaps 0;
10 US-09-864-761-31909 10 US-09-974-300-3860 10 US-09-9800-729-158 10 US-09-980-729-158 10 US-09-986-761-11427 9 US-10-040-739-710 10 US-09-974-300-5452 10 US-09-974-300-5452 12 US-10-044-090-616 12 US-10-002-775-10 12 US-10-002-775-10 13 US-09-910-616 14 US-09-913-134 16 US-09-910-664-43 17 US-09-910-664-53 18 US-09-910-664-53 18 US-09-910-664-54 19 US-09-910-664-54 10 US-09-910-64-54 10 US-09-910-33186 10 US-09-910-33186 10 US-09-910-33186 10 US-09-910-33186 10 US-09-910-3317-118 10 US-09-910-664-54 10 US-09-910-64-54 10 US-09-910-64-54 10 US-09-910-3317-118 10 US-09-910-3317-118 10 US-09-910-3317-2031 10 US-09-980-107-3327	ALIGNMENTS (709833381 020132090A1e1 Nucleic Acid US/09/833,381 4-11 4-11 6-13 6: Version 3.0	Score 18.2; DB 10; Pred. No. 14; Mismatches 4; 25
64.0 243 64.0 312 64.0 498 64.0 496 64.0 496 64.0 1074 64.0 1026 64.0 3593 64.0 4521 64.0 4521 64.0 4523 64.0 4523 64.0 4523 64.0 4523 63.2 725 63.2 725 725 725 725 725 725 725 725 725 725	RESULT 1 US-09-833-381-1755/c ; Sequence 1755, Application US/09833381 ; Patent No. US20020132090A1 ; GENERAL INFORMATION: APPLICAMY: RODISON, Keith E. TITLE OF INVERTION: No. US20020132090A1e1 Nucrement PRILE REFERENCE: 5800-119 FILE REFERENCE: 5800-119 CURRENT APPLICATION NUMBER: US/09/833,381 CURRENT APPLICATION NUMBER: 09/516,448 PRIOR FILING DATE: 2000-02-29 NUMBER OF SEQ ID NOS: 2050 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: ASSESQ for Windows Version 3.0 SOFTWARE: MAMEKEY: Misc_feature LUCATION: (1)(731) CUCATION: (1)(731) CUCATION: (1)(731)	72.8 Larity 83.3 Conservative TTGGAAGGGTAG
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PATENT NO. USZUOZULIJUSO/ALI

GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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US-09-954-456-2252
US-09-954-456-2252, Application US/09954456
; Patent No. US20020115057A1
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; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-2252
                                                                                                                                                                                                                                              NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-954-456-1357
                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 1357
LENGTH: 372
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SEQ ID NO 2252
LENGTH: 372
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   NUMBER OF SEQ ID NOS: 2276
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US-09-880-107-1971
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Patent No. US20020115057A1

GENERAL INFORMATION:

APPLICART: Young, Paul

TILLE OF INVENTION: Sets

TILLE OF INVENTION: Sets

FILE REFERENCE: 689290-76

CURRENT FILING DATE: 2000-09-18

PRIOR PLICATION NUMBER: US/60/234,052

PRIOR PLICATION NUMBER: US/60/234,052

PRIOR PLICATION NUMBER: US/60/234,052

PRIOR PLICATION NUMBER: US/60/234,052

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-25

PRIOR PLING DATE: 2000-09-26

PRIOR PLING DATE: 2000-09-27

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                      CURRENT FILLING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILLING DATE: 2000-09-18
PRIOR FILLING DATE: 2000-09-18
PRIOR FILLING DATE: 2000-09-20
PRIOR FILLING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR PILLING DATE: 2000-09-26
PRIOR FILLING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
SPRIOR PAPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
SPRIOR PALLING DATE: 2000-09-27
CURRENT APPLICATION NUMBER: US/09/954,456
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100.0%; Pre
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; OTHER INFORMATION: n=a,t,g or c
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Best Local Similarity 100.
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US-09-954-456-1357
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GENERAL INFORMATION:
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                                                    APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Schaff, Uwe
APPLICANT: Schaff, Uwe
APPLICANT: Schaff, Uwe
APPLICANT: Schaff, Uwe
APPLICANT: Schaff, Unc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFRENCE: 44221-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/217,054
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1971
LENGHI 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 72.0%; Score 18; DB 10; Best Local Similarity 100.0%; Pred. No. 15; Matches 18; Conservative 0; Mismatches 0
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ilarity 83.3%; Pred. No. 35;
Conservative 0; Mismatches
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LOCATION: (1)..(372)

OTHER INFORMATION: n = a or c or g or t
US-09-880-107-1971
Sequence 1971, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
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APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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US-10-174-590-517
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Matches 20; Conserv
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC;
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC;
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: U5/10/052,586
CURRENT FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-10-17
PRIOR PRIOR DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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APPLICANT: Wood William I.
APPLICANT: Wood William I.
APPLICANT: Annoy Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION UNMER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 517
LENGTH: 3690
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Pred. No. 35;
Sequence 517, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
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; Sequence 517, Application US/10052586
; Patent No. US20020127584A1
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Best Local Similarity 83.3%;
Matches 20; Conservative (
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Watanabe, Colin K.
Wood, William I.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
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                                                                                 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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US-10-176-758-517
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R APPLICATE: 1998-03-11
R FILING DATE: 1998-03-11
R APPLICATION UNBER: 60/078886
DR FILING DATE: 1998-03-20
OR FILING DATE: 1998-03-20
OR PLICATION NUMBER: 60/079664
OR APPLICATION NUMBER: 60/079664 R FILING DATE: 1997-12-17
R APPLICATION NUMBER: 60/068017
R FILING DATE: 1997-12-18
R FILING DATE: 1997-12-18
R FILING DATE: 1998-03-10
R FILING DATE: 1998-03-10
R APPLICATION NUMBER: 60/07/632 R APPLICATION NUMBER: 60/065311
R FILING DATE: 1997-11-13
R APPLICATION NUMBER: 60/066120
R APPLICATION NUMBER: 60/066466
R FILING DATE: 1997-11-24
R APPLICATION NUMBER: 60/066772
R APPLICATION NUMBER: 60/069335
R APPLICATION NUMBER: 60/069335
R APPLICATION NUMBER: 60/069335
R APPLICATION NUMBER: 60/069335 R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/063541 FILING DATE: 1997-10-28 APPLICATION NUMBER: 60/063544 FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063564
FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063734 APPLICATION NUMBER: 60/063870 FILING DATE: 1997-10-31 APPLICATION NUMBER: 60/069425 FILING DATE: 1997-12-12 APPLICATION NUMBER: 60/077649 FILING DATE: 1998-03-11 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 FILING DATE: 1998-03-27 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081838 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082704 APPLICATION NUMBER: 60/069870 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080327 FILING DATE: 1998-04-01 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/063540 APPLICATION NUMBER: 60/064103 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 APPLICATION NUMBER: 60/080333 APPLICATION NUMBER: 60/083496 1997-10-28 FILING DATE: 1997-10-29 1998-03-11 1997-10-3 1998-04-2 FILING DATE: ILING DATE: FILING DATE: PRIOR
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APPLICATION NUMBER: 60/083559 FILING DATE: 1998-04-29 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085573 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-05-15 FILING DATE: 1998-05-22 APPLICATION NUMBER: 60/086486 FILING DATE: 1998-05-28 APPLICATION NUMBER: 60/087208 APPLICATION NUMBER: 60/087609 FILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087759 FILING DATE: 1998-06-02 FILING DATE: 1998-06-03 APPLICATION NUMBER: 60/088025 APPLICATION NUMBER: 60/088028 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 60/088740 APPLICATION NUMBER: 60/088825 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/083499 APPLICATION NUMBER: 60/084366 APPLICATION NUMBER: 60/084414 APPLICATION NUMBER: 60/084639 60/084640 60/085579 60/085580 APPLICATION NUMBER: 60/085582 60/086023 60/086392 APPLICATION NUMBER: 60/087098 APPLICATION NUMBER: 60/088033 APPLICATION NUMBER: 60/088722 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088811 APPLICATION NUMBER: 60/088824 APPLICATION NUMBER: 60/084643 60/087827 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-04-29 FILING DATE: 1998-04-29 FILING DATE: 1998-05-05 FILING DATE: 1998-05-06 FILING DATE: 1998-05-07 FILLING DATE: 1998-05-15 APPLICATION NUMBER: 60/ FILLING DATE: 1998-05-15 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-18 FILING DATE: 1998-05-22 FILING DATE: 1998-06-04 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 1998-05-07 FILING DATE: 1998-06-04 FILING DATE: 1998-05-1 FILING DATE: 1998-05-APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: PRIOR PRIOR PRIOR PRIOR
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GREATEAL INCOMATION:

APPLICANT: GAIGAT. Alexander

APPLICANT: GAIGAT. ALEXANDER

APPLICANT: AND ALE, Paul A.

APPLICANT: AND ALGER PAUL A.

APPLICANT: MAINION, JAME

TITLE OF INVERTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THEF

TITLE OF INVERTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2017.00.1200

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/126, 479

PRIOR PILING DATE: 2000-04-27

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200, 779

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/222, 903

PRIOR PILING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: 60/222, 903

PRIOR PILING DATE: 2000-06-39

PRIOR PILING DATE: 2000-06-44

PRIOR PILING DATE: 2000-06-43

PRIOR PILING DATE: 2000-06-44

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68.0%; Score 17; DB 10; Length 578;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: EXPRESSED IN ADDLT LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOCTHWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 12703
LENGTH: 578
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OTHER INFORMATION: EXPRESSED IN ADULT
OTHER INFORMATION: EXPRESSED IN FETAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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US-09-796-692-7437/c
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1 Similarity 83.3%; Pred. No. 35;
20; Conservative 0; Mismatches 4;
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PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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                             PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08861
PRIOR APPLICATION NUMBER: 60/08863
PRIOR PILING DATE: 1998-06-11
PRIOR PELLING DATE: 1998-06-11
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/08909
PRIOR PILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089105
PRIOR PELLING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-12
PRIOR PELLING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR PRIOR DATE: 1998-06-16
PRIOR PRIOR DATE: 1998-06-16
PRIOR PRILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2135 AGGCTGGTGGGAAAGGTGCCCA 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089908
         APPLICATION NUMBER: 60/088826
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Best Local Similarity
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US-09-864-761-12703/c
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us-09-674-593-9.rnpb

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Query Match
Best Local Similarity
Matches 19; Conserv
US-09-878-574-3221
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Sequence 14812, Application US/09878574

Patent No. US200201105481

GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR PLING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

LENGTH: 264
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Sequence 3121, Application US/09878574

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: La ROSa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14

PRIOR FILING DATE: 1999-06-14

ONDHERE OF SEQ ID NOS: 15775
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                                                                                                                                                                                                                               DB 9;
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82.6%; Pred. No. 64;
Live 0; Mismatches
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                                                                                                                                                                                                                             Score 16.8;
Pred. No. 53;
SOFTWARE: FastSEQ for Windows Version 3.0
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CRGANISM: Glycine max
CTHER INFORMATION: Clone ID: 701069281H1
US-09-878-574-14812
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                                                                                                                                             ; LOCATION: (231)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-7437
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                                                                                                                                                                                                                                                                                                                                    244 GATGTTTGGACAGNGTAGCAC 224
                                                                                                                                                                                                                                                                                                            4 GCTGTTTGGAAAGGGTAGCAC 24
                                                                                                                                                                                                                             Query Match 67.2%;
Best Local Similarity 85.7%;
Matches 18; Conservative
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                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Matches 19; Conserva
                                                                                                                          NAME/KEY: unsure LOCATION: (231)
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US-09-878-574-14812
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LENGTH: 300
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18.9-99-867-19.13040 APPLICATION US/09864761

SEQUENCE 11048 APPLICATION US/09864761

PRESENT INFORMATION: SHARTON G.

APPLICANT: PERO, USCACOTOGA PERO, SHARTON G.

APPLICANT: PERO, WORNATION: HUMAN CENNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITULE OF INVENTION: HUMAN CENNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITULE OF INVENTION: HUMAN CENNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOLICATION NUMBER: US/09/64,761

CHURENT APPLICATION NUMBER: US/09/64,761

PHOROR APPLICATION NUMBER: US/09/64,761

PHOROR APPLICATION NUMBER: US/09/64,766

PHOROR APPLICATION NUMBER: US/09/64,766

PHOROR APPLICATION NUMBER: US/09/64,766

PHOROR APPLICATION NUMBER: US/09/64,766

PHOROR APPLICATION NUMBER: PCT/US01/0666

PHOROR PELLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0666

PRIOR PELLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0667

PRIOR APPLICATION NUMBER
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Length 362;
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
                                                                          Indels
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       DB 10;
Score 16.6; DE
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                          171 AGGCTGATTGGAAAGGACAGGAC 193
                                                                                                                                                 2 AGGCTGTTTGGAAAGGGTAGCAC 24
66.4%;
ilarity 82.6%;
Conservative
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Gaps

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66.4%; Score 16.6; DB 9; Length 15000; 82.6%; Pred. No. 1.4e+02; tive 0; Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                   968 AGGCTATTTGGAAAGCGGAGCCC 946
                                                                                                                                                                                                                                                                                        2 AGGCTGTTTGGAAAGGGTAGCAC 24
  SOFTWARE: PatentIn version 3.0
SEQ ID NO 175
LENGTH: 15000
                                                                                                                                                                             Query Match
Best Local Similarity 82.67
Matches 19; Conservative
                                                                          ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-175
                                                                                                                                                                                                                                                                                                                                                                      Sequence 115, Application US/09895913A

Fatent No. US2002016645A1

GENERAL INFORMATION:
APPLICANT: Rleanthous, Harold
APPLICANT: Rleanthous, Harold
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Jean Francois
APPLICANT: Tomb, Jean Francois
APPLICANT: Comen, Raymond P.
TITLE OF INVENTION: Encoding No. US20020160456A1el Helicobacter Polypeptides in the
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 115
LEAGTH: 1080
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US-09-954-531-175/c

Sequence 175, Application US/09954531

Sequence 175, Application US/09954531

Sequence 175, Application US/09954531

GENERAL INFORMATION:
APPLICAMT: Zoe

TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFRENCE: 689290-77

CURRENT APPLICATION NUMBER: US/60/234,531

CURRENT APPLICATION NUMBER: US/60/234,009

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR PILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

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Pred. No. 83;
0; Mismatches 4; Indels 0
                                                                                                        Length 520;
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.66; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1 US-09-864-761-13048
                                                                                                                                                           Indels
                                                                                                        DB 10;
                                                                                                Query Match 66.4%; Score 16.6; D
Best Local Similarity 82.6%; Pred. No. 72;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                      255 TAGGCAGTGTGAAAGAGTAGCA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              617 GCTCTTTGAAAAGGCTAACAGA 639
                                                                                                                                                                                                        1 TAGGCTGTTTGGAAAGGGTAGCA 23
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Best Local Similarity 82.6%;
Matches 19; Conservative
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; LOCATION: (101)...(1000)
US-09-895-913A-115
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US-09-895-913A-115
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Scoring table:

Searched:

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Database

Title: Perfect score:

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sequence:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

En (Dasses 1 to 879)

In (Dasses 1 to 879)

In NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Lonpublished (1999)

Email: cgapbs-remail.inh.gov

Tissue Procurement: ATCC

CONA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLCM2558 row: e column: 01

High quality sequence stop: 690.

i.cetion/Qualifiers

I. .879
                                                                                                                                                                                                                                                                                                                                                                                                879 bp mRNA linear EST 21-AUG-2002
5' mRNA sequence.
BQ553400.1 GI:22368878
EST.
                                                                    B0919757 AGENCOURT
BF139543 601785555
BE28281 601100553
BE282891 601340853
BE59229 603240853
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BE59220 603240853
BE59220 60324024
BE59200 fac0112.
BE595600 fac01112.
BE7580128
BE7680128
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BE768013 fe2600.y
BN776459 fe2600.y
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BN77641 ff2600.y
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BN77641 ff2600.y
BE71330 so60e06.y
AS33115 AS SO22A
BE11330 so60e06.y
BE11330 so60e06.y
AS97727 2M0253D12
BE611995 CT12.4_N1
BF16599 601791247
BC61995 GT12.4_N1
BF16599 601791247
BC61995 GT12.4_N1
BF16599 601791247
BC6199 601791247
BC61988 yr46h04.s1
AM14858 xe88611.x
BB790491 BB790491
       BIO81374 602893438
BIO5298 602893587
BIO81897 602877120
BM230552 K0296607-
BIG91212 603311015
BF143945 60178489
AU050911 AU050911
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                                                                     BQ919757
BF139543
BF282881
BC026713
BB057249
BB195421
BQ512701
A1477839
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BQ259600
BI743491
AW566609
BM776459
BM776416
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AQ332115
BQ170080
BE211330
AZ977273
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BF143993
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BF662899
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human.
17.1
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KEYWORDS
SOURCE
ORGANISM
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BQ953400/c
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AUTHORS
TITLE
JOURNAL
COMMENT
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BG749180 602708139
AL477353 T. brucei
AQ649802 Sheared D
AQ949417 Sheared D
AW323372 uo58e09.y
                                                           January 18, 2003, 23:34:34; Search time 1569 Seconds (without alignments) 258.054 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                           fotal number of hits satisfying chosen parameters:
                                                                                                                                                            16154066 seqs, 8097743376 residues
                                                                                                                  25
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BG749180
TA191F11Q
AQ649802
AQ949417
AW323372
                                                                                                                  taggctgtttggaaagggtagcaca
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Maximum Match 100%
Listing first 45 summaries
                                          OM nucleic - nucleic search, using sw model
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Trypanosoma.

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Trypanosoma.

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Trypanosoma.

Trypanosoma brucei genome sequencing project, Sanger Centre, The Welloome Trust Genome Campus, Hinxton, Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Welloome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GuTvat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v +i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

petails of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ649802 Sheared DNA-16K8.TR Sheared DNA Trypanosoma brucel genomic clone Sheared DNA-16K8, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trypanosoma.
1 (bases 1 to 592)
El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
                                                                                                                                                                                                                                              TA191F11Q 491 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 191f11, reverse sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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llarity 87.5%; Pred. No. 3.1e+02;
Conservative 0; Mismatches 3;
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     Pred.
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                                                                                                           783 GCTGTTTGGAAAGGGTAGCACA 762
                                                                                                                                                                                                                                                                                                     genomic survey sequence.
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AQ649802.1 GI:5142988
GSS.
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     Best Local Similarity
Matches 22; Conserv
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1 (bases 1 to 1045)

1 (bases 1 to 1045)

2 NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

L. Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

rissue Procurement: ArCc

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAL at:

http://mage.lln.gov

Plate: LCAMGRES rows n. column: 09
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Organism="Homo sapiens"

/organism="Homo sapiens"

/organism="Homo sapiens"

/dlone="INAGE:4844444"

/clone=lib="NIH_MGC_43"

/clone=lib="NIH_MGC_43"

/tissue_type="normal pigmented retinal epithelium"

/lab_host="Bl108 (phage-resistant)"

/note="Organ: eye; Vector: porB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally

cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCAGGGG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. |"
/organism="Homo sapiens"

/db xref="taxon:9606"

/clone="INAGE:6376296"

/clone="INAGE:6376296"

/tissue_type="normal pigmented retinal epithelium"

/tab_nost="DH108 (phage-resistant):

/note="Organ: eye; Vector: porB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Library constructed by Ling
in the laboratory of Gerald M. Rubin (University of
California. Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
Note: this is a NIH_MGC Library. | "
1 others
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100.0%; Pred. No. ...
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High quality sequence stop: 822.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BG749180
BG749180.1 GI:14059833
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/organism="Mus musculus"
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1 (bases I to 603)

1 (bases I to 603)

Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat

10.1 sheared DNA library
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
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                         , Fraser,C. and Adams,m.

Jetraherion of clone end sequences from Trypanosoma brucel GUTat
10.1 sheared DNA library
Unpublished (1999)
Other_GSSs: Sheared DNA-16K8.TF
                                                                                                                                                                                                                                            Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Reverse
Class: shotgun.
Location/Qualifiers
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Unpublished (1999)
Cother_GSSs. Sheared DNA-31K11.TF
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                            /organism="Trypanosoma brucel"
/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-16K8"
/clone_lib="Sheared DNA"
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AQ949417
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/organism="Trypanosoma bruce!"
/strain="Trypanosoma bruce!"
/db_xref="taxon:5691"
/db_xref="taxon:5691"
/clone="sheared DNA"
/clone="sheared DNA"
/clone="sheared DNA"
/rote="vector: pUCl8; Site_1: Smai; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce! (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making smail insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: Capbbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: NI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Tel: 301 838 0200
Fax: 301 838 0208
Email: nelsayedfujr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13 Reverse
Class: shotgun.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.lln1.gov/bbrp/image/image.html
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High quality sequence stop: 430.
Location/Qualifiers
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BASE COUNT
ORIGIN
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AUTHORS
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BI105298
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E I (bases 1 to 698)

NIH-MGC http://mgc.nci.nih.gov/.

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Emal: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Llocation/Qualifiers

Location/Qualifiers
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                                                         /clone="IMAGE:2646760"
/clone_lib="NCI_CGAP_Lu29"
/clone_lib="NCI_CGAP_Lu29"
Strissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_1: SalI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_
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Pred. No. 3.6e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 624;
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/clone="Inabs:4978802",
/clone="Inabs"NOI_GAP_Mam6"
/sex="female, virgin"
/tissue_Iype="infiltrating ductal carcinoma"
/dev_stage="5_months"
/lab_host="DH108"
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1 Similarity 87.5%; Pred. No. 3.5e+02;
21; Conservative 0; Mismatches 3;
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                                 /db_xref="taxon:10090"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 AGCCTGTTTGAAAAGGTTACCACA 259
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Best Local Similarity
Matches 21; Conserv
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BG976420
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BIO81374 100 bp mRNA linear EST 20-JUN-2001 602879438F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5010968 5',
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 751)
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://imaga.llnl.gov
                                                                                                                                                                                                                                                                             1 (bases 1 to 700)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/clone=lib="NCI_CGAP_Man2"
/tissuc_type="tumor, biopsy sample"
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/lab_host="DH108"
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87.5%; Pred. No. 3.6e+02;
iive 0; Mismatches 3;
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Location/Qualifiers
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                                                                                                            BI081374.1 GI:14499704
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BI105298
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                      house mouse
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/lab_host-"DH10B"
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house mouse.
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BM230522/c
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                                                                                                            BASE COUNT
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                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="CZECH II"
/dbraref="Laxon:10090"
/clone="IMAGE:5038677"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="Dnion"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_I: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
145 c 200 g 193 t
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E I (bases 1 to 789)

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: The 1.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI1054 row: g collumn: 05

High quality sequence stop: 725.
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         Email: cgapbs remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11106 row: n column: 22
High quality sequence stop: 741.
Location/Qualifiers
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/dev_stage="5 months"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 76.8%; Score 19.2; DB 13; Best Local Similarity 87.5%; Pred. No. 3.7e+02; Matches 21; Conservative 0; Mismatches 3;
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Contact: Robert Strausberg, Ph.D.
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BM230522 790 bp mRNA linear EST 31-JAN-2002 K0296G07-3 NIA Mouse Unfertilized Egg cDNA Library (Long) Mus musculus cDNA clone K0296G07 3', mRNA sequence.
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/lab_host="DH10B"
/note="Vector: pSPORT1 (Invitrogen); Site_1: Sall; Site_2:
Not1; Mouse cDNA project by the Laboratory of Genetics,
Not1; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nla.nlh.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
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/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"
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Plao, Y. Kargul,G.J. Dudekula,D.B., Qian,Y., Luo,A., Stagg,C.A., Martin,P., Alba,K., Tanaka,T. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
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Contact: Dawood B. Dudekula
Contact: Dawood B. Dudekula
Liaboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0296 row: G column: 07
Seq primer: -21M13 Forward
High quality sequence stop: 790
POLYAA'es.
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1 Similarity 87.5%; Pred. No. 3.8e+02;
21; Conservative 0; Mismatches 3; Indels 0
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/db_xref="taxon:10090"
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/organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: gapbs: Teminalination of the contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: gapbs: Teminalination of the contact: Robert Strausberg, Ph.D.
Tissue Procurement: Jofffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov n column: 04
High quality sequence stop: 777.
Location/Qualifiers

rce //organism="Mus musculus"
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and cloned into Sall/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 793)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 3.8e+02;
0; Mismatches 3; Indels 0
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Pred. No. 3.8e+02;
0; Mismatches 3; Indels 0
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                                                                                                                                                                                                                                                               181 AGGCTGTTTGAAAAGGTTACCACA 158
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BI691212
BI691212.1 GI:15653841
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ilarity 87.5%;
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1 Similarity 87.5%;
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/note="Organ: lung; Vector: pcNV-SPORT6; Site_1: NotI;
Site_2: SalI; transgenic model WNT-1, expression driven by
MMYV-LTR enhancer; cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM9258 row: a column: 23
High quality sequence stope: 590.
Location/Qualifiers
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BF143945 B7-2000 BF143945 B7 Z4-OCT-2000 601786489F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4014238 5',
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Sasaki, M., Suzuki, Y., Watanabe, M., Imai, J., Shibui, A., Yoshida, K., Hata, H., Yamaguchi, R., Tateyama, S. and Sugano, S.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 839)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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87.5%; Pred. No. 3.9e+02;
tive 0; Mismatches 3;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMl357 row: c column: 23
High quality sequence stop: 696.
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EST.
Email: khashi@nih.go.jp
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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January 18, 2003, 23:06:14; Search time 1670 Seconds (without alignments) 435.671 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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25
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Perfect score:
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Run on:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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EC014954 1287 bp mRNA linear PRI 04-OCT-2001 Homo sapiens, clone MGC:22980 IMAGE:4874845, mRNA, complete cds. BC014954 ALIGNMENTS BC014954.1 GI:15928979 Homo sapiens. Homo sapiens RESULT 1
BC014954/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE ORGANISM

Eukaryottoria Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1287)
Strausberg, R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian REFERENCE AUTHORS TITLE JOURNAL

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 4377)

Van Den Eyndé, B.J., Gaugler, B., Probst-Kepper, M., Michaux, L.,

Devuyst, O., Lorge, F., Weynants, P. and Boon, T.

A new antigen recognized by cytolytic T lymphocytes on a human

Widney tumor results from reverse strand transcription

J. Exp. Med. 190 (12), 1793-1800 (1999)
                                                2 (bases 1 to 1382)
Van den Eynde, B.J., Gaugler, B. and Pilotte, L.
Direct Submission
Submitted (30-MG-1999) Ludwig Institute for Cancer Research,
Avenue Hippocrate, 74, Brussels 1200, Belgium
Location/Qualifiers
1. 1382
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Submitted (30-AUG-1999) Ludwig Institute for C
Avenue Hippocrate, 74, Brussels 1200, Belgium
Location/Qualifiers
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Van den Eynde, B.J., Gaugler, B. and Pilotte, L.
  Med. 190 (12), 1793-1800 (1999)
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1754. .>2348
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AF181720.1 GI:6684526
                                                                                                                                                                                                                                                                                                                                                /gene="RU2"
738. .992
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Best Local Similarity 100.0
Matches 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 34 Row: m Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706690.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYRDNAYKDLAWKHGNIHLSAPCIYSEVMEALKLQPGLSFLNLGSGTGYLSTMVGLIL
GPFGINHGIELHSDVVEYAKEKLESFIKNSDSFDKRRSRALGAVRPLGQRRCLPTRSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELRRRPAGKMSGSSARSSHLSOPVKSVLVYRNGDPFYAGRRVVIHEKKVSSFEVFLK
EVTGGVQAPFGAVRNIYTPRTGHRIKKLDQIQSGGNYVAGGQEAFKKLK"
281 c 359 g 304 t
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                                                                                                                                                                                                                                                                         Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hslao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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1 (bases 1 to 1382)
Van Den Eynde, B.J., Gaugler, B., Probst-Kepper, M., Michaux, L., Devuyst, O., Lorge, F., Weynants, P. and Boon, T.
A new antigen recognized by cytolytic T lymphocytes on a human kidney tumor results from reverse strand transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1287
// Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:22980 IMAGE:4874845"
/fissue_type="Sye, normal, pigmented retinal epithelium"
/clone_lib="NHH MGC_43"
/lab_host="DH108-R"
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590.
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                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
BX Sequencing, by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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/product="Unknown (protein for MGC:22980)"
/protein_id="AAH14954.1"
/db_xref="GI:15928980"
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                                                                    Project URL: http://mgc.nci.nih.gov
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                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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Direct Submission
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Best Local Similarity
Matches 25; Conserv
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                                                                                                               /protein_id="AAF23611.1"
/db_xref="G1:6684528"
/translation="MDDDAAPRVEGVPVAVHKHALHDGLRQVAGPGAAAAHLPRWPPP
                                                                                                                                                                                                                                                                                                                                                                /protein_1d="AAF23610.1"
/db_xref="G1:6684527"
/translation="MSGSSARSSHLSOPVVKSVLVYRNGDPFYAGRRVVIHEKKVSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 10-JUL-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 120029)
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Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVFLKEVTGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAGGQEAFKKL'
858 c 828 g 1380 t 15 others
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2056. .>2148
/gene="RU2"
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SEQUENCING IN PROGRESS ***, 5 unordered pieces.
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25;
Pred. No.
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HTG; HTGS_PHASE1; HTGS_CANCELLED.
                            complement(1912. .2166)
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                                                         /codon_start=1
/product="RU2AS"
/product-"RU2AS"
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/product="RU25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Matches 25; Conservative
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HSJ282H10
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Submitted (01-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 3, 2001 this sequence version replaced gi:13446455.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL359713 152966 bp DNA linear PRI 01-MAY-2001
Human DNA sequence from clone RP11-95P3 on chromosome 6, complete
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152966)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                         23430 23529; gap of 100 bp 23530 63600: contig of 40071 bp in length 63601 63700: gap of 100 bp 63701 100099: contig of 36399 bp in length 100100 100199: gap of 100 bp 100200 10236: contig of 2167 bp in length 102367 102466: gap of 100 bp 102467 120029: contig of 17563 bp in length 102467 120029: contig of 17563 bp in length.
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23530. .6360.
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fragment_chain:1"
63701. .100099
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fragment_chain:1"
100200. .102366
/note="assembly_fragment:01789"
102467. .120029
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/clone_lib="RPCI-1"
1. .23429
/note="assembly_fragment:05837
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/db_xref="taxon:9606"
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Emi. EMBL; Sw:, SWISSPRCT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGF/Chr6 RPII-95P3 is from the library RPCI-11.1 constructed by the group of Pieter ac Jong. For further detablis see http://www.chori.org/Dacpac/home.htm
VECTOR: pBACe3.6 intrafer detablis see http://www.chori.org/Dacpac/home.htm
RPII-95P3 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true left end of clone RPII-95P3 is at 11700 in this sequence. The true right end of clone RPII-90P3 is at 11700 in this sequence.
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note="AluJo/FRAM repeat: matches 181. .298 of consensus"
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/note="140 copies 2 mer ga 75% conserved"
/note="LIM1 repeat: matches 1012. .159% of consensus"
5581. .5859
/note="Alusg repeat: matches 18. .294 of consensus"
5986. .6369
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/note="FLAM_C repeat: matches 1. 143 of consensus"
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'note="L2 repeat: matches 1512. .1735 of consensus"
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/note="L2 repeat: matches 2612. .2747 of consensus"
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/note="MIR repeat: matches 65. .262 of consensus"
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/hote="Alusq repeat: matches 1.
3014. .3296
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/note="match: GSS: Em:AZ517849"
24. .379
/note="match: GSS: Em:B63526"
32. .494
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/note="match: GSS: Em:AQ315706"
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/note="match: GSS: Em:B54691"
complement(9393. .9853)
/note="match: GSS: Em:AQ285817"
10311. .10437
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/note="match: GSS: Em:AQ285677"
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/note="LTR7 repeat: matches 1.
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/db_xref="taxon:9606"
/chromosome="6"
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19. .544
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/note="L2 1
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.295 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches 163. .299 of consensus 28701. .28930
/note="MLTIG repeat: matches 32. .301 of consensus" 29080 .29171
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22589. .22728
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          .309 of consensus"
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22591. .22670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement(19337. .19501)
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complement(19370. .19546)
/note="match: GSS: Em:AQ128461"
) 19566. .19739
/note="matchs repeat: matches 126. .2519740. .20100
/note="LIMD3 repeat: matches 7391 777
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complement(19269. 19546)
/note="match: GSS: Em:AQ663911"
complement(19325. 19546)
/note="match: GSS: Em:AQ021494"
complement(19337. .19501)
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           repeat: matches 1.
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19265. .19495
note="match: GSS: Em:AQ373351
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Albacoks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbzrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Benton, J., Benton, D., Boutek, J., Benton, D., Brown, E., Brown, M., Bryant, N.D., Buhay, C., Burch, P., Burkett, C., Burrell, R.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chav, R., Chen, R., David, R., David, R., David, R., Danid, M.L., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Garcia, A., Garner, T., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Hart, M., Hodues, M., Hollans, B., Hernandez, O., Hodgson, A., Hune, J., Jackson, L. E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PACLID 426 98724 bp DNA linear HTG 13-JUL-2002 Rattus norvegicus clone CH230-185A19, *** SEQUENCING IN PROGRESS ***, 52 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L2 repeat: matches 2342. .2501 of consensus"
37251. .37544
                   /note="L2 repeat: matches 2323. .2710 of consensus"
29712. .29834
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L2 repeat: matches 1836. .1959 of consensus"
35164. .35461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2710 of consensus"
                                                                      consensus,
                                                                                                                    consensus
                                                                                                                                                                                                            .208 of consensus'
                                                                                                                                                                                                                                                   /note="THEIC repeat: matches 1. 371 of consensus" 33360. 33511 /note="MIR repeat: matches 98. .250 of consensus" 34011. 13431 /note="AluSx repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  .232 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSq repeat: matches 2. .298 of consensus"
35532. .35990
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; Pred. No. 4.5;
0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="12 copies 4 mer caca 75% conserved"
38467. .38492
                                                                    /note="MLT1G repeat: matches 29. .147 of
                                                                                                                  .2252 of
                                                                                                                       /note="match: STS: Em:HSJJ7T"
30919. .3120
7.note="MERSBA repeat: matches 1.../note="matches 1...
                                                                                                             /note="L2 repeat: matches 1806.
complement(30720. .31207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 2254.
36631. .36790
                                                                                                                                                                                                                                                                                                                                                                     34621. 34732
/note="MIR repeat: matches 120.
34888. 35007
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Rattus norvegicus
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AC115426
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AC115426/c
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KEYWORDS
SOURCE
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 52 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (19-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 98724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (13-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19549134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 42669 bases at least Q40
Consensus quality: 45549 bases at least Q30
Consensus quality: 47683 bases at least Q20
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2: gap of unknown length
3: gap of unknown length
3: gap of unknown length
7: contig of 1344 bp in length
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8: gap of unknown length
1: contig of 1405 bp in length
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Worley, K.C.
Direct Submission
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Literia Bubmission Super Centre, Hinxton, Cambridgeshire, Clubmisted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clone-request@Sanger.ac.uk

On May 11, 2001 this sequence version replaced gi:13751283.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP; Information on the WORMPEP that their source databases: Em:, EMBL; Sw:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL157396 128796 bp DNA linear PRI 09-MAY-2001
Human DNA sequence from clone RP11-437J2 on chromosome 10, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 128796)
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91.7%; Pred. No. 1.9e+02;
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contig of 4072 bp
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AL157396
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Felis catus clone RP86-588L5, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-43712 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-43712 is at 128796 in this sequence. The true right end of clone RP11-30E16 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

(basea 1 to 16473)

Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q., Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Masiello, C., Mastrian, S.D., McClosky, J.C., McDowell, J., Pearson, R., Prasad, A., Shevchenko, Y., Snyder, B., Stautripop, S., Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., NISC, Comparative Sequencing Initiative
                 http://www.sanger.ac.uk/HGP/Chr10
RP11-437J2 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-MAY-2001) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Further information can be found at
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Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-437J2"
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25975 c 24235 g 37921 t
                                                                              http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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Felis catus.
Felis catus
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AC091543.1 GI:13940632
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Matches 22; Conservative
Group.
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Consensus quality: 160900 bases at least Q20
Insert size: 175000; agarose-fp
Insert size: 163673; aum-of-contigs
Quality coverage: 10.73x in Q20 bases; agarose-fp
Quality coverage: 11.47x in Q20 bases; sum-of-contigs
                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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101750. 128418
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128519. 164773
/note="assembly_fragment"
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/organism="Felis catus"
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    Worley, K.C.
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                          TITLE
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MURZAYD, M. Adamas. C., Addio-Oduola, B., Ali-osman, F.R., Allen, C., Alabracks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Benks, T., Benken, J., Benken, J., Bilmage, K., Blankenburg, K., Bonnin, D., Bunket, C., Burchl. R. L., Payant, N. E., Carron, T.F., Carter, M., Carvaca, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, G., Chen, R., Cher, G., Chen, G., Chen, R., Cher, G., Chen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M., Davila, M.L., Davis, C., Davis, Carron, T.L., Ding, Y., Dinh, H.H., Delandy, R.R., Darger, H., Dugan-Rochas, C., Durbin, K., J., Earnhart, C., Edgar, D., Flagg, N., Ford, J., Escotto, M., Farls, T., Ferraguto, D., Flagg, N., Ford, J., Escotto, M., Farls, T., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Gabisi, A., Gao, T., Garzia, N., Gall, R., Gardis, C., Harris, K., Hart, M., Hale, S., Hamilton, K., Harrandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jacobson, E., Kalls, T., Johnson, R., Johnson, W., Johnson, W., Martine, J., Johnson, W., Johnson, C., Liu, J., Liu, W., Louiseged, H., Locado, R., Martin, L., Lau, B., Martinez, E., Mahner, J., Marting, L., Marting, R., Marting, E., Mawhiner, E., Martin, R., Marting, R., Marting, M., Moris, M., Morser, M., Medu, P., Martin, R., Marting, R., Martin, M., Mapue, P., Martin, R., Marting, R., Martin, R., Marting, R., Martin, R., Marting, R., Martin, M., Mapue, P., Martin, R., Marting, R., Martin, R., Martin
                                                                                                                                                                                                                                                           ACLI/U62 168203 bp DNA linear HTG 18-JUL-2002
Rattus norvegicus clone CH230-177D13, *** SEQUENCING IN PROGRESS
***, 59 unordered pieces.
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Submitted (06-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 168203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                         Gaps
                          Length 164773;
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                      83.2%; Score 20.8; DB 2;
ilarity 91.7%; Pred. No. 1.7e+02;
Conservative 0; Mismatches 2;
                                                                                                                                             Db 36014 TAAATGGGTGGCCGGGGGGGTGA 36037
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HTG; HTGS_PHASE1.
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Unpublished
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Query Match
Best Local Similarity
Las 22; Conserv
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AC117062
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KEYWORDS
SOURCE
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 59 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Direct Submission
Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 14, 2002 this sequence version replaced gi:20066113.
Center: Baylor College of Medicine
                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 consensus quality: 103705 bases at least Q40 Consensus quality: 109417 bases at least Q20 consensus quality: 113895 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                         1556: contig of 1556 bp in length
1656: gap of unknown length
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                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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bp in length

of 1465

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NAAKAKAALARKPERKASPKFGEWQVEVVNYHFPGNRNNPIDNNDLTHRLYGYLARW
VLEGFKENEDAAQRELIKTYINPIAESNGTRWDNAAEIYLAFPGTEWFLEFENFYP
LIIGIYRVKGGMDPQYLKKALRQRYGSLTADKWMSQKTTAIAKSLKDVEQLKWGRGG
LSDTAFLQKFGIRLP
98. 391
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/translation="MASHPPVQMDLILMQGWWTSVLNMGKQLISIPLGSSSLMPQKPK
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/protein_id="CRA92805.1"
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/db_xref="SPTRMBL:088471"
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                                                                                                                                                                                                                                                                                                                                                               Virology,
                                                                                                                                                                                                                                                                                                                                                        Submitted (03-JAN-1996) Alexander Plyusnin, Department of Virology Haartman Institute, Helsinki University, Haartmaninkatu 3, Haasinki, FIN-00014, Finland
2 (bases 1 to 977)
Vapalahti, O., Plyusnin, A., Cheng, Y., Manni, T.,
Brummer-Korvenkontio, M. and Vaheri, A.
Brummer-Korvenkontio, M. and Vaheri, A.
Sequence and Pahyna, the European California serogroup bunyaviruses: sequence and phylogeny of the S RNA segment
J. Gen. Virol. 77 (Pt 8), 1769-1774 (1996)
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180 c 233 g 259 t
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1. 977 /Organism="Tahyna virus"
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                                                                                                                                                                                                                                              Viruses; SERNA negative-strand viruses; Bunyaviridae;
Orthobunyavirus
1 (bases 1 to 977)
Plyusnin,A.
Direct Submission
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Pred. No. 8.8e+02;
                                                                                                       RNA
92).
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Tahyna virus S segment RNA (strain
268497
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79. .786
/codon_start=1
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/db_xref="taxon:45270"
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Tahyna virus
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88.0%;
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Best Local Similarity 88.00,
"Thes 22; Conservative
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in length

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66 15552; contig of 693 bp in length 1555; contig of 693 bp in length 1555; contig of 693 bp in length 1555; contig of 693 bp in length 16545; contig of 693 bp in length 173 1555; gap of 100 bp in length 173 1555; gap of 100 bp in length 18129; contig of 691 bp in length 18129; contig of 691 bp in length 18129; contig of 715 bp in length 18129; contig of 715 bp in length 18129; contig of 715 bp in length 18129; contig of 719 bp in length 187 1686; gap of 100 bp in length 188 1886; contig of 681 bp in length 188 1886; contig of 684 bp in length 188 1886; gap of 100 bp in length 188 1886; gap of 100 bp in length 188 1880; contig of 684 bp in length 188 1880; gap of 100 bp in length 188 1880; gap of 18
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34116: contig of 695 bp in length

126: gap of 100 bp

14907: contig of 691 bp in length

1707: gap of 100 bp

187706: contig of 699 bp in length
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States 1 to 70905)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boquslavkly, L., Buckpalter, B., Brom, A., Colangaelo, M., Collins, S., Changai, J., Changaler, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hilme, M., Tliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landerares, R., Landers, T., Lehoczky, J., Levine, R., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Malton, J., Maneus, L., Minova, T., Norman, C., Lindelad-Toh, K., Liu, G., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Minova, T., Norman, C., McConnor, T., O'Donnell, P., O'Nell, D., O'Connor, T., O'Donnell, P., O'Nell, D., O'Connor, T., O'Donnell, P., O'Nell, D., Norman, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Stantos, R., Schauer, S., Schupback, R., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Myman, D., Ye, W.J., Young, G., Connor, A., Waman, D., Ye, W.J., Young, G., Chanker, A., and Zody, M., Zainoun, J., Zembok, L., Zimmer, A., and Zody, M., Strift, M., Marchell, M., Marchell, M., Marchell, M., Marchell, M., Marchell, M., Wann, D., Ye, W.J., Young, G., Shubisson, M., Zimmer, A., and Zody, M., Tantist, M., Marchell, M., Ma
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 70905)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-MXY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP24-239D13
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5407: contig of 6
5507: gap of 100
6196: contig of 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name: 239_D_13
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Dietrich, N.L., Eagle, W.O., Gan, W., Gupta, J., Ho, S.-L., Huang, M.C., Idol, J., Jamison, D.C., Lee-Lin, S.-Q., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., Morse, E., Ojodu, M.A., Pearson, R., Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Thongson, E.E., Touchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (20-FEB-2000) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 7.83x in Q20 bases; agarose-fp Quality coverage: 6.55x in Q20 bases; pulse-field-gel Quality coverage: 7.56x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 175245 bases at least Q40 Consensus quality: 176047 bases at least Q30 Consensus quality: 178044 bases at least Q20 Insert size: 208000; pulse-field-gel Insert size: 208000; pulse-field-gel Insert size: 208000; pulse-field-gel
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contig of 9085 bp in length
gap of unknown length
contig of 14158 bp in length
gap of unknown length
contig of 21283 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113227: contig of 57221 bp in length
gap of unknown length
180252: contig of 67025 bp in length.
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of 5498 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
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88.0%; Pred. No. 2.8e+02;
iive 0; Mismatches 3;
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1. 180252
/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
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Beckstrom-Sternberg, S.M., Benjamin, B., Bouffard, G.G.,
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Pred. No. 3.5e+02;
0; Mismatches 3; Indels 0;
07 35806: gap of 100 bp 36516: contig of 710 bp in length 17 3616: gap of 100 bp in length 18 37312: contig of 696 bp in length 18 37412: gap of 100 bp in length 42 38241: gap of 100 bp in length 42 3867: contig of 726 bp in length 8967: contig of 693 bp in length 68 39760: contig of 693 bp in length 61 3980: gap of 100 bp in length 61 3980: gap of 100 bp in length 61 3980: gap of 100 bp in length 62 40551: contig of 691 bp in length 62 40551: contig of 691 bp in length 63 41332: contig of 681 bp in length
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47738: contig of 692 bp in length
4788: gap of 100 bp
48623: gap of 100 bp
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*** SEQUENCING IN PROGRESS ***,
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Submitted (16-58P-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                            Rattus norvegicus clone CH230-9F16, 72 unordered pieces.
Db 97998 TTAGTGGTTGGGCGGGGGGGAGAC 98022
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Worley, K.C.
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docg/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 72 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                       Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 51063 bases at least 040 Consensus quality: 55683 bases at least 020 Consensus quality: 55972 bases at least 020
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Contact: hgsc-help@bcm.tmc.edu
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jóin(5499. :5597,5854. :6118,6440. :6621,7206. :7409,
7682. :7869,8444. :8606,9418. :9642,9735. :9866,10502. :10597,
10701. :11764)
/gene="PEPCK"
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Williams, C.P., Postic, C., Robin, D., Robin, P., Parrinello, J., Shelton, K., Printz, R.L., Magnuson, M.A., Granner, D.K., Forest, C. and Chalkley, R.
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(bases 1 to 12141)

Granner, C.P., Postic, C., Parrinello, J., Shelton, K., Frintz, R.L., Granner, D.K., Magnuson, M.A. and Chalkley, R.

Direct Submission

Submitted (19-JUN-1997) Molecular Physiology and Biophysics, Vanderbilt University, 21st and Garland Avenues, Nashville, TN 37232, USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene,
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/gene="PEPCK"
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MCKAY,R., Butler,M.M., Wyatt,J. and Cowsert,L.M.
Antisense modulation of pepck-cytosolic expression
Patent: US 6187545-A 10 13 FEB-2001;
Location/Qualifiers
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'Organism="Mus musculus"

/strain="129 SV"

/db_xref="taxon:10090"

/chromosome="2"

/map="103.0"

/gene="PEPCK"
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/organism="unknown"
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                                                                                                                                                                                                                                                                                                            VAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEGIDEPLAPGVTTSWKNKEWR
PODAEPCAHPNSRCTPASQCPIIDPAWESPEGVPIEGIIFGGRRPEGVPLYYEALSW
OHGVFVGAAMSEATAREHGKIIIMPPFAMRPFFGYNFGKYLAHWLSMAHRPAAKL
PKIFHVNWFKROKOGKELWPGFGENSRVLEWMFGRIEGEDSAKLTPIGYIPKSNALN
KGLGGVNVEELFGISKEFWEKEVEEIDRYLEDQVNTDLPYEIERELRALKQRISGM"
                                                                                                                                                                                                                             VPIPKTGLSQLGRWMSEEDFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLAKTGIEL
TADSPYVVASARR IMTRMGISVEBALGADGEFIKCHJUSVGCPLEKKPLYWNAKONPELTL
TAHLPDRREIISFGGGGGGGGGGGKGCAKKCPARASKLAKEEGWLARHMILLGITNPEGR
KKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKFDAQGNLRAINPENGFFG
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/number=2
join(5895. .6118,6440. .6621,7206. .7409,7682. .7869,
8444. .8606,9418. .9642,9735. .9866,10502. .10597,
10701. .11155)
/gene="PEPCK"
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/gene="PEPCK"
/number=3
7206. 7409
/gene="PEPCK"
/number=4
/number=4
/682. 7869
/gene="PEPCK"
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8444. .8606
/gene="PEPCK"
/number=6
9418. .9642
/gene="PEPCK"
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9735, .9866
/gene="PEPCK"
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10502. 10597
/gene="PEPCK"
/number=9
10701. 11764
/gene="PEPCK"
/number=10
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Best Local Similarity 91.37
Matches 21; Conservative
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                     CDS
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Search completed: January 19, 2003, 00:44:32 Job time: 1868 secs

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January 18, 2003, 22:00:24; Search time 212.5 Seconds (without alignments) 264.941 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                            4370478
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               2185239 seqs, 1125999159 residues
                                                                                                                                                                                                                                  1 taggetgtttggaaagggtageaca 25
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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25
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Perfect score:
Sequence:
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Database :	N Geneseg 101002:*
	1: /SIDS2/gcgdata/geneseq/genesegn-embl/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	PCR primer VDE120	Human tumour rejec	Non-infective Tick	Plasmid construct	Encodes Western su	Tick-borne encepha	TBE virus strain N	Murine Kit/stem ce	DNA encoding preme
SUMMARIES	AAZ36648	AAZ36643	AAT12500	AAV59451	AAN81162	AAT44469	AAT15820	AAD13425	AAX59954
DB	21	21	17	19	6	17	11	22	20
% Query & Match Length DB ID	25	1382	2181	2181	2418	11141	11141	5098	2055
% Query Match	100.0	100.0	79.2	79.2	79.2	79.2	79.2	76.8	72.8
Score	25	25	19.8	19.8	19.8	19.8	19.8	19.2	18.2
Result No.	П	0	æ	4	Ŋ	9	7	œ	σ

18.2 72.8 128139 24 AA 18.2 72.8 133719 21 AA 18.2 72.0 372 24 AB 18 72.0 372 24 AB 18 72.0 372 24 AB 17.2 3695 22 AA 17.2 2695 22 AA 17.2 2695 22 AA 17.5 70.4 3690 22 AA 17.5 68.0 578 22 AA 17.5 68.0 572 52.0 AA 17.5 68.0 52.0 AA 17.5	1	4291 RRV genome nucleot 4754 Macaca mulatta rha 4754 Cana #1971 med to	Lung cancer	Lung cancer		9567 Human expressed po	Boving		Нишал	HUIIBII		Нишап	Human	Hullian	1252 Probe #9938 used t	Human genome-de	cDNA sequence	Regulator O		Human	Himan	Human				0484 Hepatoma AS-30D Ty			, 11	ALIGNMENTS						RUR-1 antisense cDNA sequence.	E	ij												
18.2 72.8 128139 18.2 72.8 133719 18 72.0 372 18 72.0 372 18 72.0 372 18 72.0 372 17.8 71.2 3685 17.6 70.4 3902 17.6 70.4 3902 17.6 70.4 43902 17.6 70.4 43902 17.6 68.0 578 18.6 67.2 679 16.8 67.2 679 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 16.8 67.2 5150 17.6 68.0 578		∀ ⊬ <	. 4	4 4	. m	~ <	. 4	α.	4 -	٦ ،	9	٦,	~ (v c	4 (4	4	4,	۰.	4. (40			~	8	m	œ :	α.	4 (ρ 4	AL	ď	,				amplify									. 44	. 8		Ä		
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141 4236 2-FE 2-FE 2-FE 3-MA 3-MA 11 D		200	2	00			10	0	0	$-\infty$	00	8	യ	0 0	၁ထ	æ	00 0	D C	o o	oα	œ	œ	8	8	æ	^	^	~ r	- 9		ر د د د د د د د د د د د د د د د د د د د	1		0 (f	,		human	PCR p	•	0		A1.	c	M			. !			053076
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Matches 25; Conserv
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08-JUL-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                 AAT12500;
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                                                                                                                                                                                                                                                                                                                                        RESULT 3
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                                                   PCR primers AA226647-48 were used to amplify the antisense cDNA sequence of human tumour rejection antigen RUR-1. The RUR-1 antisense sequence is the antisense strand of a ubiquitously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal cell carcinoma, colorectal carcinoma, melanoma, sarcoma or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "binding site for primer VDE120 (see AAZ36648)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            site for primer VDE119 (see AAZ36647)"
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated tumour rejection antigen RUR-1 nucleic acids, used for, e.g. treatment of cancers - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; human; tumour rejection antigen; RUR-1; tumour; cancer; renal cell carcinoma; colorectal carcinoma; melanoma; sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tumour rejection antigen RUR-1 antisense cDNA sequence.
                                                                                                                                                                                                                                                               DB 21; Length 25;
                                                                                                                                                                                                                                                  100.0%; Score 25; DB 21; Lengua 2. 100.0%; Pred. No. 0.017; Vismatches 0; Indels
                                                                                                                                                                                                                                Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1280..1305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
738..992
                           Example 1; Page 44; 75pp; English.
                                                                                                                                                                                                                                                                                                                         1 TAGGCTGTTTGGAAAGGGTAGCACA 25
                                                                                                                                                                                                                                                                                                                                                   1 TAGGCTGTTTGGAAAGGGTAGCACA 25
                                                                                                                                                                                                                                                                                                                                                                                                             AA236643/c
ID AA236643 standard; cDNA; 1382 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 5; 75pp; English
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e.g. treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
523..547
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P-PSDB; AAY53809.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ36643;
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
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The present sequence represents the antisense cDNA sequence of human tumour rejection antigen RUR-1. The present sequence is the antisense strand of a ubiquitously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line IB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal calcinoma, colorectal carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/note= "encodes N-terminal region of non-structural protein NSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= C_(residues_86..116)
/note= "encodes C-terminal region of core protein"
2074..2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tick-borne encephalitis virus; TBE virus; vaccine; non-infective; Flavivirus; membrane-associated protein E; prM; subviral particle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-infective Tick-borne encephalitis virus construct pSV-PEwt.
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                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 21; Length 1382; 100.0%; Pred. No. 0.033;
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 1382 BP; 355 A; 373 C; 344 G; 310 T; 0 other;
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/note= "prM = 94..360; M = 361..585"
586..2073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1304 TAGGCTGTTTGGAAAGGGTAGCACA 1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tick-borne Encephalitis Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT12500 standard; DNA; 2181
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94AT-0001352.
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/*tag= a
94..585
/*tag= b
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Gaps

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This sequence encodes a novel plasmid construct, SV-PEwt which is used in a method for the production of a vaccine against flavivirus infections. The construct comprises nucleic acid encoding flavivirus proteins E and prw/M in full-length native form. The vaccine is used especially for vaccination against tick-borne encephalitis (TBE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA and RNA mols encoding proteins of meningoencephalitis virus -
useful in vaccines, diagnostic agents and detection probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Encodes Western subtype of early summer meningoencephalitis (ESME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Encodes all the structural proteins of ESME virus. The invention covers fragments of this sequence and analogous RNA molecules. Corresponding mRNA sequence given in specification.
                                                                                                                                                                                DB 19; Length 2181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               early summer meningoencephalitis virus; live vaccines; ds
                                                                                                                                                                                                                      Indels
                                                                                                                                              Sequence 2181 BP; 558 A; 450 C; 688 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2418 BP; 635 A; 507 C; 743 G; 533 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAP80573, AAP82324, AAP82325 & AAP82326
                                                                                                                                                                              Score 19.8; DI
Pred. No. 11;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Early summer meningoencephalitis virus
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728..952
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113..460
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/product=protein C
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953..2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-protein E
 Example 1; Fig 3A-C; 34pp; German.
                                                                                                                                                                                                                                                                           900 TGGACTGTTTGGAAAGGGTAGCA 922
                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                      1 TAGGCTGTTTGGAAAGGGTAGCA 23
                                                                                                                                                                                                                                                                                                                                                                                  AAN81162 standard; DNA; 2418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heinz FX, Kunz C, Mandl C,
                                                                                                                                                                              Query Match 79.2%;
Best Local Similarity 91.3%;
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                        parts of the TBE virus sequence coding for proteins E and prM+M were amplified using PCR. Sequence analysis of the amplified fragments showed that most contained mutations. One clone which encoded full-length pratein E in their wild-type forms. The combined coding insert was incorporated into commercially available vector pSybeta from which the beta-galactosidase gene and part of the polylinker had been removed. The resulting construct was designated pSy-PEW and was sultable for liposome-mediated transfection of COS-1 cells. The cells were cultured to produce subviral particles for use in a vaccine to protect mice against TBE virus infection. The present sequence is that of the TBE-derived insert of plasmid pSy-PEWt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; contruct; plasmid; SV-PEwt; flavivirus; infection; PrM/M;
tick-borne encephalitis; TBE; E protein; ss.
                                 Vaccine for protection against tick borne encephalitis virus comprises non-infectious subviral particles contg. at least the complete E protein in native form, or nucleic acid encoding this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine against flavivirus infection, especially tick-borne encephalitis - comprises full-length native protein E and prM/M coding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19.8; DB 17; Length 2181; Pred. No. 11; D: Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2181 BP; 558 A; 451 C; 686 G; 486 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900 TGGACTGTTTGGAAAGGGTAGCA 922
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                                                                                                                            Example 1; Fig 3; 34pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid construct SV-PEwt DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 79.2%;
Local Similarity 91.3%;
les 21; Conservative
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P-PSDB; AAR88714
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28-JUL-1994;
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Gaps
                                         encoding tick borne encephalitis virus RNA - useful for vaccine
                                                                                                                                       The infectious TBEV nucleic acid can be modified to trigger prodn. of attenuated TBEV which can be used to produce a vaccine. The DNA pref. has at least one modification that reduces virulence and/or affects replication, esp. an additional G ahead of position 1, a modification at the prM cleavage site, a modification at a N-glycosylation site, one of a large number of point mutations of the TBEV E protein.
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/*tag= c
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"nucleotide illegible in the specification"
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"nucleotide illegible in the specification"
                                                                                                                                                                                                                                                                                                                                                                 Length 11141;
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"nucleotide illegible in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TBE virus; tick-borne encephalitis virus; Neudorfl;
                                                                                                                                                                                                                                                                                                                                                                   DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tick-borne encephalitis virus strain Neudorfl.
                                                                                                      Claim 1; Page 64-69 and Fig 5; 126pp; German
                                                                                                                                                                                                                                                                                                                                                                   79.2%; Score 19.8; E 91.3%; Pred. No. 15; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TBE virus strain Neudorfl complete genome
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133..10377
/*tag= a
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2040
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8160
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2100
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misc_difference 8400
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  Length 2418;
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                      encephalitis virus; TBEV; vaccine; virulence;
                                                                                                                                                                                                                                                                                                                                                Tick-borne encephalitis virus nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site"
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      DB 9;
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1207
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/note= "start of protein NS2B'
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Score 19.8; DI
Pred. No. 11;
0; Mismatches
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                                                                                                                                                                                                                           DNA; 11141 BP
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  79.2%;
91.3%;
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                                                                                                                                                                                                                           AAT4469 standard;
                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMO) IMMUNO AG
                                                                                                                                                                                                                                                                                                                                                                                                             replication;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-1995;
                                                                                                                                                                                                                                                                                                         04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                      Tick-borne
                                                                                                                                                                                                                                                                   AAT44469;
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_RNA
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                                       Matches
                                                                                                                                                                                                        AAT44469
                                                                                                                                                                                 RESULT
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fertility defect in a male, comprises detecting the presence of a con-phosphorylated tyrosine residue in the kinase insert region of a con-phosphorylated tyrosine residue in the kinase insert region of a kit/Stem cell factor receptor (SCF-R) (designated as Kit/SCF-R or Kit), or a mutation in the nucleic acid or polynuclectide encoding the CKIT/SCF-R. The presence of such mutation or non-phosphorylation indicates a fertility defects in males. The Kit inhibiting agents are suitable as for incorporation into pharmaceuticals to treat subjects in need of spermatogenesis inhibiting germ cell proliferation during cancer therapy. The Kit enhancing agents may be used to promote spermatogenesis to chance fertility in males suffering from a Kit-mediated fertility defect. The genetically altered mice are useful models for sterility testing in a mammal. The present sequence is a cDNA encoding mutine kinase insert region of Kit/SCF-R.
       /*tag= a
/product= "Murine Kit/stem cell factor receptor kinase
insert region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying a fertility defect in a male, comprises detecting the presence of mutation or a non-phosphorylated tyrosine residue in the kinase insert region of a Kit/Stem cell factor receptor \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Premembrane protein; envelope protein; antigen; DNA vaccine; viral tick-borne encephalitis; cross-protection; Russian spring summer encephalitis virus; Central European encephalitis virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5098 BP; 1309 A; 1224 C; 1235 G; 1330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding premembrane and envelope antigenic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
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                                                                                                                                                                                                                                                                                             (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Central european encephalitis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 46-47; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3956 AGGCTGTTTGAAAAGGTTACCACA 3979
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                                                                                                                                                                                               08-JAN-2001; 2001WO-US00573
                                                                                                                                                                                                                                               11-JAN-2000; 2000US-0175625
                                                                                                                                                                                                                                                                                                                                              Blume-Jensen P, Hunter T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-AUG-1999 (first entry)
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Best Local Similarity
`~hes 21; Conserve
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-502588/55.
P-PSDB; AAE07144.
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                                                                                                                                                 19-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
/*noie= "nucleotide illegible in the specification"
8460
                                                                       /*note= "nucleotide illegible in the specification" misc_difference 8520
                                                                                                                                                                                                                        /*tag= n
/*note= "nucleotide illegible in the specification"
                                                                                                                             /*tag= m
/*note= "nucleotide illegible in the specification"
misc_difference 8580
                                                                                                                                                                                                                                                                                             /*tag= o
/*note= "nucleotide illegible in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The new complete DNA encoding tick borne encephalitis virus RNA may be used to produce infectious viral particles. These particles may be use in vaccines (live attenuated or inactivated), opt. formulated with an immunomodulator. These virus particles are also useful as seed for viral replication. The new cDNA is also useful itself as a vaccine.

The sequence is the first complete TBEV sequence known and makes possible targeted alteration of the viral genome (partic. for attenuation or increasing viral yields).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete DNA encoding tick borne encephalitis virus RNA - able to produce infectious viral particles for use in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.2%; Score 19.8; DB 17; Length 11141; Best Local Similarity 91.3%; Pred. No. 15; Matches 21; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine Kit/stem cell factor receptor kinase insert region cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11141 BP; 2820 A; 2455 C; 3526 G; 2326 T; 14 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
29..2956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1287 TGGACTGTTTGGAAAGGGTAGCA 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD13425 standard; cDNA; 5098 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 5; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mandl C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94DE-4426622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-106416/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heinz FX, Kunz C,
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                                                misc_difference
                                                                                                                                                                                                                                                                    misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                  DE4426622-C1
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Gaps

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Indels

Length 5098;

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/note= "has similarity to KSHV interleukin (IL)-6 gene" complement (20777..21778)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /hote= "has similarity to KSHV K4 viral MIP gene" 26846..27409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= u
/label= RRV_ORF24
/note= "has similarity to KSHV ORF24"
                                                                                                                                                                                                                                        /*tag= i
/label= RRV_ORF11
/note= "has similarity to KSHV ORF11"
complement (19921..20544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Product= "thymidine kinase"
/label= RRV_ORF21
/note= "has similarity to KSHV ORF21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= t
/label= RRV_ORF23
/note= "has similarity to KSHV ORF23"
complement (37123..39321)
                                                                                                                                                                                                                                                                                                                                                                                     /product= "thymidylate synthase"
/label= RRV_ORF70
/note= "has similarity to KSHV ORF70"
complement (22245..22592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "has similarity to KSHV ORF16" complement (27515..29125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= RRV_ORF18
/note= "has similarity to KSHV ORF18"
complement (29905...31548)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= RRV_ORF19
/note= "has similarity to KSHV ORF19"
complement (31043..32095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= q
/label= RRV_ORF20
//note= "has similarity to KSHV ORF20"
32094..33767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "glycoprotein H"
/label= RRV_ORF22
/note= "has similarity to KSHV ORF22"
complement (35865..37073)
                                                                                                                                                                                   /label= RRV_ORF10
/note= "has similarity to KSHV ORF10"
18520..19749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORF17
                                                                                                        /product= "DNA polymerase protein"
/label= RRV_ORF9
/note= "has similarity to KSHV ORF9"
17261..18511
                                         /product= "glycoprotein B"
/label= RRV_ORFB
/note= "has similarity to KSHV ORFB"
14122..17166
'note= "has similarity to KSHV ORF7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= RRV_ORF17
/note= "has similarity to KSHV
28998..29897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= p
/product= "tegument protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "Bcl2-homologue"
                                                                                                                                                                                                                                                                                                        /*tag= j
/product= "RRV R2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "RRV R3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- RRV_ORF16
                                                                                                                                                                                                                                                                                                                        /label= RRV_ORF
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               11515..14004
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/note= "has similarity to Kaposi's sarcoma-associated
virus (KSHV) open reading frame (ORF) 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRV; rhesus rhadinovirus; japanese macaque virus; multiple sclerosis; JMHV: cytostatic; antiasthmatic; antialleagic; dermatological; vulnerary; gene therapy; leucopenia; thrombocytopaenia; inflammatory disease; asthma; allergy; dermatitis; virus; ds.
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                        The present sequence encodes premembrane and envelope antigenic proteins. The sequence is used in a DNA vaccine to protect against viral tick-borne encephalitis. The vaccines induce cross-protection (humoral, cell-mediated or mucosal) against both Russian spring summer and Central European encephalitis viruses.
                                                                                                                                                                                                                                                                                                                                            Ouery Match
72.8%; Score 18.2; DB 20; Length 2055;
Best Local Similarity 87.0%; Pred. No. 63;
Matches 20; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                Sequence 2055 BP; 523 A; 427 C; 641 G; 464 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "complement binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "has similarity to KSHV ORF6" 9468..11528
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/note= "has similarity to KSHV ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/product= "dihydrofolate reductase"
                                                                         (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "transport protein"
/label= RRV_ORF7
                                                                                                                                                                 DNA vaccine against tick-borne flaviviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ssDNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2692..3258)
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/*tag= a
/product= "RRV R1"
                                                                                                                                                                                              Claim 3; Page 48-49; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI64291 standard; DNA; 128139 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                      864 TGGACTTTTGGAAAGGGTAGCA 886
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                                                                                                                                                                                                                                                                                                                                                                                                        1 TAGGCTGTTTGGAAAGGGTAGCA 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRV genome nucleotide sequence.
                  98WO-US25322,
                                              97US-0065750
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                                                                                                                                     WPI; 1999-347616/29.
                                                                                                          Schmaljohn CS;
                  20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI64291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
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ID AAI6
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46905..47135
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444433..45242
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/note= "has similarity to KSHV ORF39"
/***
           /product= "major capsid protein"
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/note= "has similarity to KSHV ORF25"
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/note= "has similarity to KSHV ORF32"
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                                                                                                           /note- "has similarity to KSHV ORF28"
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                                                                                                                                                                                       to KSHV ORF31"
                                                                                                                                                                                                                                          /note= "has similarity to KSHV ORF33"
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                                                                                                                                                                                                                                                                                                                       to KSHV ORF35
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                                                                                  to KSHV ORF27
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45408..45683
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/note= "has similarity to
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/note= "has similarity
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/note= "has similarity
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/note= "has similarity
47683..49077
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                                                                                                                                                                                                                       ..50059
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39323..43459
                                                                                                         /note= "has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Macaca mulatta rhadinovirus 1757; RRV; rhesus macaque rhadinovirus; genome; Kaposi's sarcoma-associated herpesvirus; KSHV; interleukin 6; IL-6; macrophage inflammatory protein; MIP; diagnosis; vaccine; cytostatic; anti-HIV; gene therapy; infection; Kaposi's sarcoma: lymphoproliferative disorder; B-cell hyperplasia; lymphadenopathy; splenomegaly; hypergammaglobinulinaemia; autoimmune haemolytic anaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 18.2; DB 24; Length 128139;
Pred. No. 1.38+02;
0; Mismatches 3; Indels 0;
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/note= "has similarity to KSHV ORF43"
                                                                                                        /label- RRV_ORF41
/note- "has similarity to KSHV ORF41"
complement (58525..59343)
                                                                                                                                                                                                                                                 /note= "has similarity to KSHV ORF42"
complement (59297..61027)
"has similarity to KSHV ORF40"
                                                                                 /product- "helicase/primase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wong SW, Axthelm MK, Searles RP;
                                                                                                                                                                                                                          /label= RRV_ORF42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC64754 standard; DNA; 133719 BP
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  /note= "has s
57917..58528
                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.8%;
Llarity 87.0%;
Conservative
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98US-0109409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity
20; Conserv
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the efficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarcoma, lymphoproliferative disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly, hypergammagiobinulinaemia or autoimmune haemolytic anaemia, by administering the drug to a immuno-compromised non-human primate macaque monkey obtained by as a result of infection by Sinian immunodeficiency Virus (SIV). RRV is useful for producing non-human primate model for testing potential treatments for conditions associated with RRV infection. It is also useful for testing the efficacy of the candidate vaccine against RRV infection or conditions associated with its infection by administering the vaccine to the subject capable of infection with RRV, inoculating the subject with RRV and observing the effect of vaccine. AAAG64765 and AAB53205 to AAB53213 represent sequence used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.3e+02;
0; Mismatches 3; Indels 0; 0
                                                                                                                                                                                                                                                                                                                              Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;
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87.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene #1971 used to diagnose liver cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1971; 298pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33061 GGCTGGTGGAAACGGTAGCACA 33083
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                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
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                                                                                                                                                                                                                                                                                           present invention
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                                                                                                                                                                                                                                                                                                                                            Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                      the printed
expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efflicacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                     Gaps
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                                                                                                            Score 18; DB 24; Length 372;
Pred. No. 59;
                                                                                                                                     Indels
                                                                                     Sequence 372 BP; 119 A; 55 C; 67 G; 118 T; 13 other;
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                                                                                                                                                                                                                                                                                                                       Lung cancer related gene sequence SEQ ID NO:3419.
                                                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                       100.0%; Pred. No. 59;
Live 0; Mismatches
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2000US-209531P.
2000US-233133P.
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2000US-234052P.
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2000US-234567P.
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                                                                                                                                                            1 TAGGCTGTTTGGAAAGGG 18
                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                     18; Conservative
                                                                                                                        Local Similarity
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20-SEP-2000;
20-SEP-2000;
20-SEP-2000;
22-SEP-2000;
22-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
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ABL65082
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30-MAY-2001; 2001WO-US10838
    The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (S) selected from 844 sequences set, where (I) comprises a sequence (S) selected from 844 sequences (given in ABLG1664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer.

Cosophageal, ovarian, kidney, prostate or pancreatic cancer.

Cosophageal, ovarian, kidney, prostate or pancreatic cancer.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                        Horrigan S;
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                                                                                                                                                                                                                                       determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma and Wilm's tumour
                                                                                                                                                      Ebner R,
                                                                                                                                                                                                                                                          Claim 1; SEQ ID 3419; 44pp; English
                                                                                                                                                      Carter KC,
                       02-0CT-2000; 2000US-237316P.
03-0CT-2000; 2000US-237425P.
03-0CT-2000; 2000US-23759BP.
03-0CT-2000; 2000US-237604P.
03-0CT-2000; 2000US-237606P.
01-0CT-2000; 2000US-237606P.
01-NOV-2000; 2000US-244867P.
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Soppet DR, Weaver Z;
                                                                                                                                (AVAL-) AVALON PHARM.
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in AbiGl664 to ABIG1010), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical curvature and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, cesophageal, ovarian, kidney, prostate or pancreatic cancer.
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Weaver 2;
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2000US-237425P

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Search completed: January 18, 2003, 23:46:12 Job time: 256.5 secs
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adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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59;
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The present invention describes a method (MI) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 847 sequences (given in ABL61664 CC comprises in at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening CC activity and can be used in gene therapy. MI can be used for screening CC anti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a cresult of MI, and the data is sufficient to convey the chemical CC structure and/or properties of the agent. MI can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, cosophageal, ovarian, kidney, prostate or pancreatic cancer.

CC infiltrating lobular cancer, squamous cell cancer, infiltrating ductal cancer, infiltrating ductal cancer.
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Best Local Similarity 100.
Matches 18; Conservative
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01-NOV-2000;
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Soppet DR,
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Human prostate exp Human prostate exp

AAC58017 ABV25168 ABV37980

AAA40516 AAI60823

Human protein HP10 Murine adult splee

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January 18, 2003, 22:00:24; Search time 212.5 Seconds (without alignments) 264.941 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              nucleic search, using sw model
                                                                                                                                                                                                                                             IDENTITY_NUC Gapor 10.0 , Gapert 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                           US-09-674-593-8
25
                                                                                                                                                                                                                                                                                                                                 Potal number of
                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                               Scoring table:
                                                                               OM nucleic
                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database
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ALIGNMENTS

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Human secreted pro Oligonuclectide fo Human NS cDNA sequ DNA encoding novel Human immune syste

AAC08438 ABQ48008 ABQ48009 ABQ45844

AAS92512 AAS83590

Human testicular a Human testicular a Genomic sequence # Human digestive sy Genomic sequence # Human digestive sy Human tumour suppr

ABL97850 ABL97851 AAS39928 AAK90372

AAL04957 AAL04 AAS25

Human tumour suppr Human tumour suppr

AAS39926 AAK90370 ABK12810 ABK12808 AAC30165 ABQ41640

Human reproductive Human testicular a

Human reproductive

Human testicular a Human testicular a Human cDNA encodin

Human cancer relat Human reproductive

Human

AAL06126 AAL06127 ABL98691 ABL98692

Homo sapiens 20q13 reproductive

polynucleoti Human polynucleoti Human polynucleoti

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human; tumour rejection antigen; RUR-1; tumour; cancer; carcinoma; colorectal carcinoma; melanoma; sarcoma;
                                                                  PCR primer VDE119 used to amplify RUR-1 antisense cDNA sequence
                                                                                                                                                                                                                                   Boon-Falleur T;
                                                                                                                                                                                                                 (LUDW-) LUDWIG INST CANCER RES
                AAZ36647 standard; cDNA; 25
                                                                                                                                                                                                 98US-0085318
                                                                                                                                                                                 99WO-US10424
                                                  (first entry)
                                                                                                     PCR primer; ss.
                                                                                                                                                                                                                                   /an Den Eynde B,
                                                                                                                               Homo sapiens.
                                                                                                                                                                                 13-MAY-1999;
                                                                                                                                               409958546-A1
                                                                                                                                                                                                 13-MAY-1998;
                                                  22-FEB-2000
                                                                                                                                                                18-NOV-1999
                                                                                     Antisense;
                                                                                                      leukaemia;
                                                                                             renal cell
                                                                                                                     Synthetic
                                 AAZ36647;
RESULT 1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

New isolated tumour rejection antigen RUR-1 nucleic acids, used for,

WPI; 2000-053076/04

Human polynuciecti Arachidonic acid m
AA236643 AA188448 AAF62854 AAC57997 AAC57998 AAC57999 AAC51999

12141 1000 1000 1000 1000 9594

PCR primer VDE119

Description

DB

Length

Query Match 90

Score

Result Š. Drosophila melanog

N

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AAI88448;
                                                                                                                                         Query Match
                                                                                                                                                           Matches
                                                                                                                                                                                                                              RESULT 3
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                                  PCR primers AA226647-48 were used to amplify the antisense cDNA sequence of human tumour rejection antigen RUR-1. The RUR-1 antisense sequence is the antisense strand of a ubiquitoualty expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour-derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line LB9211 RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal cell carcinoma, melanoma, sarcoma or leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1280..1305)
/*tag= c
/note= "binding site for primer VDE120 (see AAZ36648)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site for primer VDE119 (see AAZ36647)"
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated tumour rejection antigen RUR-1 nucleic acids, used for,
                                                                                                                                                                                                                                                                                                                                                            Antisense; human; tumour rejection antigen; RUR-1; tumour; cancer; renal cell carcinoma; colorectal carcinoma; melanoma; sarcoma; leukaemia; ss.
                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                           Human tumour rejection antigen RUR-1 antisense cDNA sequence.
                                                                                                                                                                           Score 25; DB 21; Length 25; Pred. No. 0.46;
                                                                                                                                                                                               Indels
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                                                                                                                                                       Sequence 25 BP; 5 A; 2 C; 14 G; 4 T; 0 other;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      Socation/Qualifiers
                  Example 1; Page 44; 75pp; English.
                                                                                                                                                                                                                  25
                                                                                                                                                                                                                          1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Den Eynde B, Boon-Falleur T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/note= "binding
                                                                                                                                                                                              ;
                                                                                                                                                                                                                 1 TAAATGGGTGGGCGGTGGGGGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                 AAZ36643 standard; cDNA; 1382
                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 5; 75pp; English.
e.g. treatment of cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0085318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US10424
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                                                                                                                                                                        Query Match
Best Local Similarity 100.(
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                        22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          ಗ
                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
523..547
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                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09958546-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                                                     AAZ36643;
                                                                                                                                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchne; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
The present sequence represents the antisense cDNA sequence of human tumour rejection antisen RUR-1. The present sequence is the antisense strand of a ubiquitously expressed gene. The antisense strand codes for a polypeptide which is preferentially expressed in tumour samples and tumour derived cells lines. The polypeptide is unrelated to any TRAP protein. The sequence was isolated from a renal cell carcinoma line LB9211-RCC. The RUR-1 nucleic acids and polypeptides can be used for diagnosis, prognosis or treatment of a disorder characterized by the expression of a RUR-1 antisense cDNA molecule or an expression product, such as cancers, e.g. renal cell carcinoma, colorectal carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 21; Length 1382; 100.0%; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 8508; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1382 BP; 355 A; 373 C; 344 G; 310 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 8508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  523 TAAATGGGTGGGCGGTGGGGGAAC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-514838/56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAO08517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
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(first entry)

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detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eloosanoid-related bialielic marker; 12-LO-related bialielic marker; ds.
                                                                                                                                                                                            Arachidonic acid metabolism related genomic biallelic marker #631.
                                                                                                                                                                                                                                  Human; biallelic marker; arachidonic acid metabolism;
                                                                             AAC57997 standard; DNA; 1000 BP.
                                                                                                                                                                                                                                                                                                                                                                                     40200047771-A2
                                                                                                                                                                                                                                                                                                                                                   Homo saptens.
                                                                                                                                                       25-JAN-2001
                                                                                                                   AAC57997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                           RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence was used in an example illustrating an invention relating to antisense compounds, compositions and methods for modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic (PEPCK-cytosolic). Antisense compounds of up to 30 nucleobases in length that are capable of inhibiting the expression of PEPCK-cytosolic are provided. The antisense compounds are useful for inhibiting the expression of PEPCK-cytosolic are expression of PEPCK-cytosolic in cells or tissues. They are commonly used as research reagents and in diagnostics, e.g. to elucidate the function of particular genes. They are also useful for distinguishing
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antisense compound capable of modulating the expression of phosphoenol pyruvate carboxykinase-cytosolic, useful for preventing or delaying infection, inflammation or tumor formation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between functions of various members of a biological pathway and for research use. The antisense compounds are also useful prophylactically, e.g. to prevent or delay infection, inflammation or tumour formation.
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.2%; Score 19.8; DB 22; Length 12141; 91.3%; Pred. No. 68;
                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; antiinflammatory; cytostatic; antisense gene therapy; phosphoenol pyruvate carboxykinase-cytosolic; PEPCK-cytosolic; infection; inflammation; tumour formation; ds.
                                                                                                                   Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12141 BP; 3122 A; 2924 C; 3087 G; 3008 T; 0 other;
                                                                                                                                                       0; Indels
                                                                             Sequence 339 BP; 84 A; 72 C; 135 G; 48 T; 0 other;
                                                                                                                   DB 22;
49;
                                       at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowsert LM;
                                                                                                                                                         Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse PEPCK-cytosolic nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 13; Column 55-70; 64pp; English.
                                                                                                                   Score 20;
Pred. No.
                                                                                                                   80.0%,
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                            AAF62854 standard; DNA; 12141 BP
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                                                                                                                                                                                                                287 GGGTGGGCGTGGGGGAGAC 306
                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JAN-2000; 2000US-0488671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-0488671.
                                                                                                                 80.08;
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                          6 GGGTGGGCGGTGGGGGAGAC
                                                                                                               Ouery Match 80.09
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Butler MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-190979/19.
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es 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2001,
                                                                                                                                                                                                                                                                                                                                                                 AAF62854;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                        RESULT 4
AAF62854/c
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Matches
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The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genes involved in arachidonic acid metabolism and from genemic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an elcosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the exemplification of the present invention.

N. B. Polymorphic bases (single nucleotide polymorphisms also known as SNPS) in the polymucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism \dot{\ }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19.2; DB 21; Length 1000; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1000 BP; 210 A; 291 C; 291 G; 207 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                      Chumakov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 754-755; 802pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204 AAATGGTGGGCGGGGGGGAGAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC57998 standard; DNA; 1000 BP
                                                                                                                                                                                                                                                                                                                                      Bougueleret L,
                                                                                                                           99US-0119917.
99US-0275267.
99US-0133200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.8%;
87.5%;
                                                                 11-FEB-2000; 2000WO-IB00184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-571881/53.
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Best Local Similarity
                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                      Blumenfeld M,
                                                                                                                                  12-FEB-1999;
                                                                                                                                                                                                   07-MAY-1999;
17-AUG-2000.
                                                                                                                                                                    23-MAR-1999;
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8237 TAAATGGGAGGGAGGTGGGGGGG 8215

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1 TAAATGGGTGGGCGGTGGGGGAG 23

Conservative

AAC57998;

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The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions involved in arachidonic acid metabolism and invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an eicosanoid related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to
                                                                                                                                  detection; hybridisation; phenotype; haplotype; SND; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or I has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism -
                                                                                 Arachidonic acid metabolism related genomic biallelic marker #632
                                                                                                                    Human; biallelic marker; arachidonic acid metabolism; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%; Score 19.2; DB 21; Length 1000; llarity 87.5%; Pred. No. 1.1e+02; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1000 BP; 224 A; 292 C; 272 G; 211 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 755; 802pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGGTGGGGGGGGGGGGAGAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blumenfeld M, Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC57999 standard; DNA; 1000
                                                                                                                                                                                                                                                                                                                                                                                  99US-0275267.
                                                                                                                                                                                                                                                                                                                                                                   99US-0119917
                                                                                                                                                                                                                                                                                                                                 11-FEB-2000; 2000WO-IB00184
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                                                  (first entry)
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                                                                                                                                                                                                                                                               WO200047771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                   2-FEB-1999;
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1999;
07-MAY-1999;
                                                25-JAN-2001
                                                                                                                                                                                                                                                                                                17-AUG-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
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The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an elcosanoid-related biallelic marker (ERBM) or 12-10-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24019 containing and AAB24019 containing and AAB24019 and AAB24019 and AAB24019 containing and AAB24019 and AAB
                                                      Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM; eicosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. Polymorphic bases (single nucleotide polymorphisms also known as SNPs) in the polynucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Arachidonic acid metabolism related genomic biallelic marker #633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.2; DB 21;
Pred. No. 1.1e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chumakov I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC58000 standard; DNA; 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.8%;
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99US-0133200.
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                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-1999;
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23-MAR-2001; 2001WO-US09231
                                    23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                              /enter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes polynucleotides including biallelic markers derived from genes involved in arachidonic acid metabolism and from genes involved in arachidonic acid metabolism and from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an eicosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC57367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the exemplification of the present invention.

N.B. Polymorphic bases (single nucleotide polymorphisms also known as SNPs) in the polymucleotide sequences from the present invention have been given as their corresponding degenerate bases e.g. a polymorphic
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specific amplification assay; identification; ERBM; 12-LO-RBM;
elcosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
                                                                                                                                                                                                                                                    Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 25664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
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Pred. No. 1.1e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1000 BP; 222 A; 299 C; 265 G; 213 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                        Chumakov I;
                                                                                                                                                                                                                                                                                       Claim 13; Page 757; 802pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 AAATGGTGGGGGGGGGGGGGAAC 33
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                                                                                                                                                                                                        Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL10394 standard; cDNA; 9594
                                                                                                                               99US-0119917.
99US-0275267.
99US-0133200.
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ilarity 87.5%;
Conservative
                                                                                                         11-FEB-2000; 2000WO-IB00184.
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                                                                                                                                                                                                                             WPI; 2000-571881/53.
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Best Local Similarity
Matches 21; Conserva
                                                          WO200047771-A2
                                                                                                                                                                                (GEST ) GENSET
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                                                                                                                                                                                                        Blumenfeld M,
                                     Homo sapiens.
                                                                                                                                             23-MAR-1999;
07-MAY-1999;
                                                                                                                                 12-FEB-1999;
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                                                                                  17-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           elcosanoid-related biallelic marker; 12-LO-related biallelic marker; ds.
                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; identification; ERBM; 12-LO-RBM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arachidonic acid metabolism related genomic biallelic marker #651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9594;
                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 25664; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blumenfeld M, Bougueleret L, Chumakov I;
                                                            Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3005 AAATGGGTGGCGGTGCCGCGCGC 3028
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                                                            Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76.8%;
87.5%;
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99US-0275267.
99US-0133200.
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                                                            Adams M,
                                                                                                                      2001-656860/75
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Best Local Similarity
(PEKE ) PE CORP NY
                                                                                                                                                          P-PSDB; ABB66291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200047771-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1999;
07-MAY-1999;
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for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-AUG-2001
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              ABV37980
                                                                                                                                                                                                           patient;
                                                                                                                                                                                                                                                                                  Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                            ABV37980
δ
                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                    from genomic regions flanking those genes. Methods from the present invention may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used to select individuals for clinical trials and predict responses to treatment with drugs. The polynucleotides may be used in hybridisation assays, sequencing assays and specific amplification assays for identifying an eicosanoid-related biallelic marker (ERBM) or 12-LO-related biallelic marker, and for amplifying a segment of nucleotides containing an ERBM. The polynucleotides are useful in diagnostic kits. The markers may be used to detect conditions and genotypes associated with arachidonic acid metabolism. AAC53367 to AAC58018 and AAB24019 and AAB24020 represent sequences used in the exemplification of the present invention.

S. B. Polymorphic bases (single nucleotide polymorphisms also known as been given as their corresponding degenerate bases e.g. a polymorphic base of C or T has been given as Y.
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                 Novel biallelic markers useful for detecting conditions and genotypes associated with arachidonic acid metabolism - \,
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                               The present invention describes polynucleotides including biallelic
                                                                                                                                                                                                                                                                                                                                          76.8%; Score 19.2; DB 21; Length 20674; 87.5%; Pred. No. 1.2e+02; cive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                   Sequence 20674 BP; 5400 A; 5170 C; 4995 G; 5062 T; 47 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 25159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                     Claim 67; Page 790-796; 802pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan
                                                                                                                                                                                                                                                                                                                                                                                          2 AAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABV25168 standard; cDNA; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2001; 2001WO-US05171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                  21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endege WO,
           WPI; 2000-571881/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                           Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV25168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
ABV25168/c
                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                  in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                             cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.4%; Score 18.6; DB 23; Length 335; 84.0%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 335 BP; 85 A; 82 C; 76 G; 82 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 37971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 7763; 11750pp; English.
Claim 1; Page 4916; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; cytostati
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV37980 standard; cDNA; 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-183319P.
2000US-189862P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200160860-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-2000;
16-MAR-2000;
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09-JUN-2000;
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13-DEC-2000;
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Gaps

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Indels

22; Length 1087;

Score 18.6; DB 22, Pred. No. 1.9e+02; 0; Mismatches 4.

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human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of ligands and receptors.
                                                                     Sequence 1087 BP; 246 A; 304 C; 288 G; 249 T; 0 other;
                                                                                                                                                                                                       921 TAAAGGGGTGGGAGGAGAGAC 897
                                                                                                                                                                      1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TAAATGGGTGGGCGGTGGGGGAGAC
                                                                                                    Query Match
74.4%;
Best Local Similarity 84.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442661/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB10244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200037630-A1
                                                                                                                                                                                                                                                                                                                                                           16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Si
Matches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ×
                                                                                                                                                                                                                                                                                                                        AAA40516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs
                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                         AAA40516,
     8×8888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a human protein coding sequence. The human protein, preferably originated from tumour cell line, is applicable as a drug, a reagent for studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein originated from tumor cell line, applicable as drug, reagent for studying intracellular protein networks and protein source for drug screening, also encoded cDNA for gene diagnosis and gene
                                                                                   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                      assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                        Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
                                  monitoring the progression of prostate cancer in a patient, assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                    74.4%; Score 18.6; DB 23; Length 469; llarity 84.0%; Pred. No. 1.8e+02; Conservative 0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                   Sequence 469 BP; 104 A; 108 C; 120 G; 137 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Pages 169-171; 471pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein HP10149 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                     397 TAAAGGGGTGGGAGGTGGAGGAAAC 421
                                                                                                                                                                                                                                                                                                                                        1 TAAATGGGTGGGCGGTGGGGGAGAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH68547 standard; cDNA; 1087
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99JP-0346864.
2000JP-0031062.
2000JP-0034090.
2000JP-0035829.
2000JP-0071161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene therapy; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saeki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000WO-JP08631
                                                    (c) assessing the ef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-381646/40.
P-PSDB; AAG93262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kato S, Eguchi C,
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200142302-A1
                                                                                                    in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-FEB-2000;
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14-FEB-2000;
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                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH68547;
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                      patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
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                                                                                                                                                                                                                                                            Secreted protein; cytostatic; immunostimulatory; antimicrobial; antiviral; immunosuppressive; antiniflammatory; vulnerary; cytokine; cell proliferation; differentiation; regulator; treatment; tumor; autoimmune disease; inflammatory disorder; wound; microbial infection; viral disease; graft versus host reaction suppression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted human proteins AS296-11 and AS34-11, useful for treating tumors, autoImmune diseases, inflammatory disorders, wounds, microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel secreted human proteins (I) which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ပ်
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Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins-Racie LA,
                                                                                                                                                                                                 Murine adult spleen cDNA fragment AE402_11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 225-226; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LaVallie ER,
Bowman MR;
BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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infections and viral diseases
AAA40516 standard; cDNA; 1089
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84.08;
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                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC.
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905 TAAAGGGGTGGGAGGAGGAGAC 881

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system classed neuropathse and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and the suppression activity, arthritis and inflammation, leukaemias and the suppression and constant activity, arthritis and inflammation, leukaemias and the suppression and constant activity.
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                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humtington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, W
Zhang J;
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1098 BP; 245 A; 287 C; 308 G; 258 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen R, Ma Y,
Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4812; 10078pp; English.
                                                                                                                                           Human polynucleotide SEQ ID NO 4812.
                                AAI60823 standard; cDNA; 1098 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Asundi V, Ch
Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0598042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0727344
                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                    leukaemia; ss
                                                                                                                                                                                                                                                                                                       Homo sapiens
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09-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
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                                                                                                        22-OCT-2001
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Wang J, V
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Zhao QA,
                                                                   AA160823;
RESULT 15
                  AAI60823
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Gaps

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ch 74.4%; Score 18.6; DB 22; Length 1098; L Similarity 84.0%; Pred. No. 1.9e+02; 21; Conservative 0; Mismatches 4; Indels 0;

Query Match Best Local Similarity

Matches

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1 TAAATGGGTGGGCGGTGGGGGAGAC 25
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